

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:10:04 ; Search time 68.5294 Seconds
(without alignments)
202.471 Million cell updates/sec

Title: US-10-749-522-8
Perfect score: 85
Sequence: 1 VHEPHEFRHVALNPV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	51	60.0	849	2	Q54XC3	DICDI	Q54xc3 dictyosteli
2	47	55.3	1043	2	Q2NNR2	LEIBR	Q2nnr2 leishmania
3	45	52.9	218	2	Q3K645	PSEPF	Q3k645 pseudomonas
4	45	52.9	218	2	Q2XGZ9	PSEPU	Q2xgz9 pseudomonas
5	45	52.9	345	2	Q4JWS4	CORJK	Q4jws4 corynebacte
6	44.5	52.4	181	2	Q41EV6	9BACI	Q41ev6 exiguobacte
7	44.5	52.4	868	2	Q6K7N9	ORYSA	Q6k7n9 oryza sativ
8	44.5	52.4	995	2	Q6K7P0	ORYSA	Q6k7p0 oryza sativ
9	44	51.8	217	2	Q48DB5	PSE14	Q48db5 pseudomonas
10	44	51.8	217	2	Q4ZMX7	PSEU2	Q4zmx7 pseudomonas
11	44	51.8	266	2	Q8FSX8	COREF	Q8fsx8 corynebacte
12	44	51.8	519	2	Q2TW73	ASPOR	Q2tw73 aspergillus
13	44	51.8	944	2	Q4UHB1	THEAN	Q4uhb1 theileria a
14	44	51.8	2180	2	Q5B489	EMENI	Q5b489 aspergillus
15	43	50.6	292	2	Q568A9	BRARE	Q568a9 brachydanio

16.	43	50.6	294	2	Q47TN4_THEFY	Q47tn4 thermobifid
17	43	50.6	325	2	Q58IN5_9ACTO	Q58in5 streptomyce
18	43	50.6	380	2	Q41SI9_FERAC	Q41si9 ferroplasma
19	43	50.6	433	2	Q5AY89_EMENI	Q5ay89 aspergillus
20	43	50.6	582	2	Q55N28_CRYNE	Q55n28 cryptococcu
21	43	50.6	582	2	Q5KBF7_CRYNE	Q5kb7 cryptococcu
22	43	50.6	583	2	Q740E5_MYCPA	Q740e5 mycobacteri
23	43	50.6	586	1	PYRG_MYCBO	P0a5u3 mycobacteri
24	43	50.6	586	1	PYRG_MYCTU	P0a5u2 mycobacteri
25	43	50.6	605	2	Q65VA6_MANSM	Q65va6 mannheimia
26	43	50.6	636	2	Q3GI16_CHLVI	Q3gil6 prosthecoch
27	43	50.6	733	2	Q60JD4_CAEBR	Q60jd4 caenorhabdi
28	43	50.6	778	2	Q7QC12_ANOGA	Q7qc12 anopheles g
29	43	50.6	1358	2	Q30C85_9REOV	Q30c85 operophtera
30	42	49.4	87	2	Q650T0_ORYSA	Q650t0 oryza sativ
31	42	49.4	134	2	Q35C32_9BRAD	Q35c32 bradyrhizob
32	42	49.4	225	2	Q4TDL5_TETNG	Q4tdl5 tetraodon n
33	42	49.4	236	2	Q5QUS9_IDILO	Q5qus9 idiomarina
34	42	49.4	246	2	Q40NS7_DESAC	Q40ns7 desulfuromo
35	42	49.4	266	2	Q8NF60_HUMAN	Q8nf60 homo sapien
36	42	49.4	277	2	Q7UKR4_RHOB	Q7ukr4 rhodopirell
37	42	49.4	298	2	Q82FC5_STRAW	Q82fc5 streptomyce
38	42	49.4	325	2	Q3F6Z1_9BURK	Q3f6z1 burkholderi
39	42	49.4	342	2	Q4SR00_TETNG	Q4sr00 tetraodon n
40	42	49.4	366	2	Q61FM3_CAEBR	Q61fm3 caenorhabdi
41	42	49.4	485	2	Q3KDP9_PSEPF	Q3kdp9 pseudomonas
42	42	49.4	502	2	Q6YZN3_ORYSA	Q6yzn3 oryza sativ
43	42	49.4	529	2	Q4E549_TRYCR	Q4e549 trypanosoma
44	42	49.4	781	2	Q440Z5_SOLUS	Q440z5 solibacter
45	42	49.4	841	2	Q2WRI3_CLOBE	Q2wri3 clostridium
46	42	49.4	935	2	Q5AXG4_EMENI	Q5axg4 aspergillus
47	42	49.4	939	2	Q4W9N5_ASPFU	Q4w9n5 aspergillus
48	42	49.4	988	2	Q9P3H7_NEUCR	Q9p3h7 neurospora
49	42	49.4	1005	2	Q4IPN4_GIBZE	Q4ipn4 gibberella
50	42	49.4	1372	2	Q4I8F4_GIBZE	Q4i8f4 gibberella
51	41	48.2	145	2	Q4PEC5_USTMA	Q4pec5 ustilago ma
52	41	48.2	191	2	Q9C9T5_ARATH	Q9c9t5 arabidopsis
53	41	48.2	213	2	Q89GB2_BRAJA	Q89gb2 bradyrhizob
54	41	48.2	217	2	Q889R2_PSESM	Q889r2 pseudomonas
55	41	48.2	223	2	Q6M4J9_CORGL	Q6m4j9 corynebacte
56	41	48.2	239	2	Q8NPN2_CORGL	Q8nnp2 corynebacte
57	41	48.2	255	2	Q8N9S2_HUMAN	Q8n9s2 homo sapien
58	41	48.2	266	2	Q8NL70_CORGL	Q8nl70 corynebacte
59	41	48.2	267	2	Q8Y296_RALSO	Q8y296 ralstonia s
60	41	48.2	271	2	Q6ABN5_PROAC	Q6abn5 propionibac

Search completed: August 14, 2006, 15:15:43

Job time : 115.529 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:12:05 ; Search time 20 Seconds
 (without alignments)
 72.163 Million cell updates/sec

Title: US-10-749-522-8
 Perfect score: 85
 Sequence: 1 VHEPHEFRHVALNPV 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : PIR_80:*
 1: pirl:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Match	Query Length	DB ID	Description
1	45	52.9	168	1	PAECGA	phosphatidylglycer
2	43	50.6	586	2	B70503	probable pyrG prot
3	42	49.4	988	2	T51054	related to alpha-a
4	41	48.2	191	2	A96765	hypothetical prote
5	41	48.2	298	2	H98170	myo-inositol catab
6	41	48.2	298	2	AE3116	myo-inositol catab
7	41	48.2	313	2	H87731	protein W10C8.1 [i
8	41	48.2	622	2	S17402	parasporal crystal
9	41	48.2	907	2	T04820	aconitate hydratas
10	40	47.1	253	2	F84845	hypothetical prote
11	40	47.1	816	2	S46268	ataxin-1 - human
12	39	45.9	141	2	C83529	hypothetical prote
13	39	45.9	142	2	T46542	hypothetical prote

14	39	45.9	280	2	B81100	2-dehydro-3-deoxyp
15	39	45.9	280	2	G81840	2-dehydro-3-deoxy-
16	39	45.9	316	2	B49702	hypothetical prote
17	39	45.9	359	2	A95277	hypothetical prote
18	39	45.9	424	1	HMIHCC	hemagglutinin-este
19	39	45.9	612	2	I73633	gene trkC protein
20	39	45.9	674	2	F82844	oligopeptidase A X
21	39	45.9	713	2	F82822	NADH-ubiquinone ox
22	39	45.9	898	2	T10101	aconitate hydratas
23	39	45.9	1488	2	T02856	probable membrane
24	38	44.7	180	2	C97050	phage related prot
25	38	44.7	214	2	S39831	hypothetical prote
26	38	44.7	233	2	C96709	hypothetical prote
27	38	44.7	263	2	T29199	hypothetical prote
28	38	44.7	420	2	D87545	cation efflux syst
29	38	44.7	440	2	H95373	probable NreB prot
30	38	44.7	513	2	AB2504	hypothetical prote
31	38	44.7	519	2	D82522	type I restriction
32	38	44.7	531	2	T44803	type I site-specif
33	38	44.7	531	2	T09460	type I site-specif
34	38	44.7	531	2	T30323	type I site-specif
35	38	44.7	633	2	D32053	parasporal crystal
36	38	44.7	704	2	S21911	BRcore-NS-Z3 prote
37	38	44.7	764	2	S49849	aconitate hydratas
38	38	44.7	905	2	T23229	hypothetical prote
39	38	44.7	1020	2	D83679	hypothetical prote
40	38	44.7	1201	2	G86441	unknown protein [i
41	37.5	44.1	1141	2	T05068	hypothetical prote
42	37.5	44.1	1165	2	T15279	hypothetical prote
43	37.5	44.1	1819	2	T26533	hypothetical prote
44	37	43.5	74	2	AH2331	50S ribosomal prot
45	37	43.5	149	1	GGWN2C	globin IIC, extrac
46	37	43.5	220	1	QQBE49	BALF1 protein - hu
47	37	43.5	222	2	AE3114	hypothetical prote
48	37	43.5	224	2	H84829	hypothetical prote
49	37	43.5	227	2	A95238	hypothetical prote
50	37	43.5	234	2	B98102	L-ribulose-phospha
51	37	43.5	244	2	JC7299	transformer-2-like
52	37	43.5	262	2	AB3545	toluenesulfonate z
53	37	43.5	269	2	T22443	hypothetical prote
54	37	43.5	270	2	H98172	amino acid ABC tra
55	37	43.5	314	2	G71974	probable keto-acid
56	37	43.5	314	2	H64531	phosphoglycerate d
57	37	43.5	336	2	T39669	probable cinnamoyl
58	37	43.5	374	2	AF1280	probable exonuclea
59	37	43.5	393	2	AG2246	hypothetical prote
60	37	43.5	404	2	C71538	hypothetical prote

Search completed: August 14, 2006, 15:16:57
Job time : 41 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:20:06 ; Search time 17.9412 Seconds
(without alignments)
56.277 Million cell updates/sec

Title: US-10-749-522-8
Perfect score: 85
Sequence: 1 VHEPHEFRHVALNPV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	44.5	52.4	868	6	US-10-449-902-36512	Sequence 36512, A
2	42	49.4	502	6	US-10-449-902-54007	Sequence 54007, A
3	41	48.2	105	6	US-10-449-902-39504	Sequence 39504, A
4	41	48.2	454	6	US-10-449-902-29549	Sequence 29549, A
5	39	45.9	294	7	US-11-056-355B-64758	Sequence 64758, A
6	39	45.9	319	7	US-11-056-355B-64757	Sequence 64757, A
7	39	45.9	345	7	US-11-056-355B-64756	Sequence 64756, A
8	39	45.9	370	7	US-11-174-307B-2998	Sequence 2998, Ap
9	39	45.9	565	6	US-10-449-902-43212	Sequence 43212, A

10	38	44.7	146	7	US-11-056-355B-90573	Sequence 90573, A
11	38	44.7	146	7	US-11-056-355B-94329	Sequence 94329, A
12	38	44.7	227	7	US-11-375-414-136	Sequence 136, App
13	38	44.7	233	7	US-11-056-355B-90572	Sequence 90572, A
14	38	44.7	233	7	US-11-056-355B-94328	Sequence 94328, A
15	38	44.7	364	7	US-11-056-355B-2976	Sequence 2976, Ap
16	38	44.7	413	7	US-11-056-355B-2975	Sequence 2975, Ap
17	38	44.7	450	7	US-11-056-355B-2974	Sequence 2974, Ap
18	38	44.7	531	6	US-10-953-349-37173	Sequence 37173, A
19	38	44.7	1127	7	US-11-056-355B-46398	Sequence 46398, A
20	38	44.7	1191	7	US-11-056-355B-46397	Sequence 46397, A
21	38	44.7	1201	7	US-11-056-355B-46396	Sequence 46396, A
22	37.5	44.1	95	7	US-11-056-355B-57741	Sequence 57741, A
23	37.5	44.1	97	7	US-11-056-355B-57740	Sequence 57740, A
24	37.5	44.1	120	6	US-10-953-349-16348	Sequence 16348, A
25	37.5	44.1	190	6	US-10-953-349-16347	Sequence 16347, A
26	37.5	44.1	307	6	US-10-449-902-51738	Sequence 51738, A
27	37.5	44.1	586	6	US-10-449-902-52760	Sequence 52760, A
28	37	43.5	69	6	US-10-953-349-25347	Sequence 25347, A
29	37	43.5	73	6	US-10-953-349-25346	Sequence 25346, A
30	37	43.5	87	7	US-11-056-355B-7885	Sequence 7885, Ap
31	37	43.5	87	7	US-11-056-355B-11876	Sequence 11876, A
32	37	43.5	128	7	US-11-056-355B-7884	Sequence 7884, Ap
33	37	43.5	128	7	US-11-056-355B-11875	Sequence 11875, A
34	37	43.5	134	6	US-10-953-349-25345	Sequence 25345, A
35	37	43.5	192	6	US-10-953-349-1611	Sequence 1611, Ap
36	37	43.5	192	7	US-11-056-355B-38410	Sequence 38410, A
37	37	43.5	192	7	US-11-056-355B-103797	Sequence 103797,
38	37	43.5	192	7	US-11-056-355B-115036	Sequence 115036,
39	37	43.5	199	6	US-10-953-349-1610	Sequence 1610, Ap
40	37	43.5	199	7	US-11-056-355B-38409	Sequence 38409, A
41	37	43.5	199	7	US-11-056-355B-103796	Sequence 103796,
42	37	43.5	199	7	US-11-056-355B-115035	Sequence 115035,
43	37	43.5	223	6	US-10-449-902-34605	Sequence 34605, A
44	37	43.5	224	6	US-10-953-349-1609	Sequence 1609, Ap
45	37	43.5	224	7	US-11-056-355B-38408	Sequence 38408, A
46	37	43.5	224	7	US-11-056-355B-103795	Sequence 103795,
47	37	43.5	224	7	US-11-056-355B-115034	Sequence 115034,
48	37	43.5	271	7	US-11-056-355B-17214	Sequence 17214, A
49	37	43.5	287	6	US-10-449-902-32722	Sequence 32722, A
50	37	43.5	291	7	US-11-056-355B-17213	Sequence 17213, A
51	37	43.5	301	7	US-11-056-355B-8863	Sequence 8863, Ap
52	37	43.5	396	7	US-11-056-355B-17212	Sequence 17212, A
53	37	43.5	455	7	US-11-056-355B-50054	Sequence 50054, A
54	37	43.5	477	7	US-11-056-355B-50053	Sequence 50053, A
55	37	43.5	534	7	US-11-056-355B-13954	Sequence 13954, A
56	37	43.5	534	7	US-11-056-355B-18290	Sequence 18290, A
57	37	43.5	548	7	US-11-056-355B-13953	Sequence 13953, A
58	37	43.5	548	7	US-11-056-355B-18289	Sequence 18289, A
59	37	43.5	1148	7	US-11-247-437-6	Sequence 6, Appli
60	36.5	42.9	317	7	US-11-293-697-3930	Sequence 3930, Ap

Search completed: August 14, 2006, 15:25:02

Job time : 22.1912 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:19:11 ; Search time 74.4118 Seconds
(without alignments)
93.375 Million cell updates/sec

Title: US-10-749-522-8
Perfect score: 85
Sequence: 1 VHEPHEFRHVALNPV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	85	100.0	15	3	US-09-808-037-8	Sequence 8, Appli
2	85	100.0	15	4	US-10-162-889-8	Sequence 8, Appli
3	85	100.0	15	4	US-10-384-788-8	Sequence 8, Appli
4	85	100.0	15	4	US-10-618-856-8	Sequence 8, Appli
5	85	100.0	15	4	US-10-622-087-89	Sequence 89, Appl
6	85	100.0	15	5	US-10-749-522-8	Sequence 8, Appli
7	85	100.0	15	6	US-11-073-526-8	Sequence 8, Appli
8	52	61.2	74	4	US-10-425-115-273531	Sequence 273531,
9	45	52.9	12	4	US-10-706-391-24	Sequence 24, Appl
10	45	52.9	12	4	US-10-706-391-25	Sequence 25, Appl
11	45	52.9	12	4	US-10-706-391-28	Sequence 28, Appl

12	45	52.9	267	5	US-10-450-763-54537	Sequence 54537, A
13	44.5	52.4	872	4	US-10-437-963-119587	Sequence 119587,
14	44	51.8	50	4	US-10-424-599-269977	Sequence 269977,
15	43	50.6	408	4	US-10-437-963-122937	Sequence 122937,
16	43	50.6	543	4	US-10-282-122A-62808	Sequence 62808, A
17	43	50.6	583	4	US-10-282-122A-61811	Sequence 61811, A
18	43	50.6	586	4	US-10-282-122A-64598	Sequence 64598, A
19	43	50.6	1148	4	US-10-259-194A-278	Sequence 278, App
20	43	50.6	1536	5	US-10-498-428-2	Sequence 2, Appli
21	43	50.6	1731	4	US-10-437-963-105727	Sequence 105727,
22	43	50.6	6238	4	US-10-343-710-71	Sequence 71, Appl
23	42	49.4	87	4	US-10-437-963-150467	Sequence 150467,
24	42	49.4	94	3	US-09-764-891-3085	Sequence 3085, Ap
25	42	49.4	94	4	US-10-205-428-271	Sequence 271, App
26	42	49.4	285	4	US-10-425-114-71586	Sequence 71586, A
27	42	49.4	285	4	US-10-425-115-321529	Sequence 321529,
28	42	49.4	298	4	US-10-156-761-11864	Sequence 11864, A
29	42	49.4	353	4	US-10-437-963-121434	Sequence 121434,
30	42	49.4	485	6	US-11-188-298-9870	Sequence 9870, Ap
31	42	49.4	502	4	US-10-437-963-169378	Sequence 169378,
32	42	49.4	634	6	US-11-067-557-168	Sequence 168, App
33	42	49.4	634	6	US-11-067-557-176	Sequence 176, App
34	42	49.4	885	4	US-10-433-802-8	Sequence 8, Appli
35	41	48.2	123	4	US-10-437-963-190370	Sequence 190370,
36	41	48.2	155	4	US-10-767-701-48753	Sequence 48753, A
37	41	48.2	190	4	US-10-425-114-50570	Sequence 50570, A
38	41	48.2	205	6	US-11-055-822-548	Sequence 548, App
39	41	48.2	205	6	US-11-055-822-1128	Sequence 1128, Ap
40	41	48.2	224	6	US-11-055-822-546	Sequence 546, App
41	41	48.2	224	6	US-11-055-822-1126	Sequence 1126, Ap
42	41	48.2	239	3	US-09-738-626-5459	Sequence 5459, Ap
43	41	48.2	255	4	US-10-104-047-3876	Sequence 3876, Ap
44	41	48.2	255	6	US-11-072-512-3876	Sequence 3876, Ap
45	41	48.2	266	3	US-09-738-626-6904	Sequence 6904, Ap
46	41	48.2	311	4	US-10-767-701-39873	Sequence 39873, A
47	41	48.2	357	4	US-10-425-114-69939	Sequence 69939, A
48	41	48.2	363	4	US-10-425-114-42461	Sequence 42461, A
49	41	48.2	384	4	US-10-425-115-219332	Sequence 219332,
50	41	48.2	401	4	US-10-425-114-50173	Sequence 50173, A
51	41	48.2	462	4	US-10-425-114-51448	Sequence 51448, A
52	41	48.2	517	4	US-10-437-963-106387	Sequence 106387,
53	41	48.2	573	4	US-10-425-114-40721	Sequence 40721, A
54	41	48.2	579	4	US-10-425-114-56872	Sequence 56872, A
55	41	48.2	579	4	US-10-425-115-216734	Sequence 216734,
56	41	48.2	625	4	US-10-428-961-48	Sequence 48, Appl
57	41	48.2	759	4	US-10-080-334-236	Sequence 236, App
58	41	48.2	764	4	US-10-080-334-80	Sequence 80, Appl
59	41	48.2	804	4	US-10-080-334-235	Sequence 235, App
60	41	48.2	834	4	US-10-176-306-11	Sequence 11, Appl

Search completed: August 14, 2006, 15:24:16
Job time : 91.4118 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:15:15 ; Search time 34.4118 Seconds
(without alignments)
38.154 Million cell updates/sec

Title: US-10-749-522-8
Perfect score: 85
Sequence: 1 VHEPHEFRHVALNPV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	85	100.0	15	2	US-09-830-954A-8	Sequence 8, Appli
2	45	52.9	443	2	US-09-489-039A-10246	Sequence 10246, A
3	44	51.8	804	2	US-09-252-991A-21676	Sequence 21676, A
4	41	48.2	192	2	US-09-605-703B-2524	Sequence 2524, Ap
5	41	48.2	255	2	US-10-104-047-3876	Sequence 3876, Ap
6	41	48.2	353	2	US-09-252-991A-26103	Sequence 26103, A
7	41	48.2	431	2	US-09-489-039A-14276	Sequence 14276, A
8	41	48.2	623	2	US-09-041-991A-6	Sequence 6, Appli
9	41	48.2	623	2	US-09-608-533A-6	Sequence 6, Appli
10	41	48.2	625	2	US-09-661-322A-48	Sequence 48, Appli

11	41	48.2	633	2	US-09-041-991A-8	Sequence 8, Appli
12	41	48.2	633	2	US-09-041-991A-10	Sequence 10, Appl
13	41	48.2	633	2	US-09-608-533A-8	Sequence 8, Appli
14	41	48.2	633	2	US-09-608-533A-10	Sequence 10, Appl
15	41	48.2	1596	2	US-09-328-352-5542	Sequence 5542, Ap
16	40	47.1	273	2	US-09-252-991A-17447	Sequence 17447, A
17	40	47.1	314	2	US-09-248-796A-18946	Sequence 18946, A
18	40	47.1	659	2	US-09-252-991A-17731	Sequence 17731, A
19	40	47.1	789	2	US-10-207-706-5	Sequence 5, Appli
20	40	47.1	792	2	US-10-207-706-4	Sequence 4, Appli
21	40	47.1	816	1	US-08-267-803B-9	Sequence 9, Appli
22	40	47.1	816	2	US-09-041-886-17	Sequence 17, Appl
23	40	47.1	816	2	US-09-538-092-1208	Sequence 1208, Ap
24	40	47.1	816	2	US-10-207-706-3	Sequence 3, Appli
25	39	45.9	84	1	US-08-359-705B-41	Sequence 41, Appl
26	39	45.9	84	1	US-08-286-846A-41	Sequence 41, Appl
27	39	45.9	84	1	US-08-457-880A-41	Sequence 41, Appl
28	39	45.9	84	2	US-08-444-622A-41	Sequence 41, Appl
29	39	45.9	84	2	US-09-156-923-41	Sequence 41, Appl
30	39	45.9	149	2	US-09-252-991A-29051	Sequence 29051, A
31	39	45.9	612	1	US-08-359-705B-8	Sequence 8, Appli
32	39	45.9	612	1	US-08-286-846A-8	Sequence 8, Appli
33	39	45.9	612	1	US-08-457-880A-8	Sequence 8, Appli
34	39	45.9	612	2	US-08-444-622A-8	Sequence 8, Appli
35	39	45.9	612	2	US-08-942-562-8	Sequence 8, Appli
36	39	45.9	612	2	US-09-156-923-8	Sequence 8, Appli
37	39	45.9	1399	2	US-08-462-467B-14	Sequence 14, Appl
38	38	44.7	69	2	US-09-248-796A-24357	Sequence 24357, A
39	38	44.7	199	2	US-09-482-273-205	Sequence 205, App
40	38	44.7	227	2	US-09-774-639-155	Sequence 155, App
41	38	44.7	316	2	US-09-252-991A-27084	Sequence 27084, A
42	38	44.7	357	2	US-09-252-991A-32564	Sequence 32564, A
43	38	44.7	376	2	US-09-248-796A-19334	Sequence 19334, A
44	38	44.7	402	2	US-09-489-039A-12788	Sequence 12788, A
45	38	44.7	473	2	US-09-328-352-5279	Sequence 5279, Ap
46	38	44.7	609	2	US-09-252-991A-32547	Sequence 32547, A
47	38	44.7	633	2	US-09-186-002-18	Sequence 18, Appl
48	38	44.7	634	2	US-09-186-002-2	Sequence 2, Appli
49	38	44.7	2584	2	US-08-936-135-4	Sequence 4, Appli
50	38	44.7	2588	2	US-08-936-135-2	Sequence 2, Appli
51	38	44.7	3218	1	US-08-764-100-27	Sequence 27, Appl
52	37.5	44.1	458	2	US-10-029-180-100	Sequence 100, App
53	37	43.5	94	2	US-09-345-236B-15	Sequence 15, Appl
54	37	43.5	140	2	US-09-949-002-440	Sequence 440, App
55	37	43.5	215	2	US-09-252-991A-32685	Sequence 32685, A
56	37	43.5	234	2	US-09-583-110-4749	Sequence 4749, Ap
57	37	43.5	236	2	US-09-107-433-3704	Sequence 3704, Ap
58	37	43.5	242	2	US-09-902-540-16132	Sequence 16132, A
59	37	43.5	307	2	US-09-328-352-7631	Sequence 7631, Ap
60	37	43.5	308	2	US-09-265-585C-102	Sequence 102, App

Search completed: August 14, 2006, 15:18:35

Job time : 48.4118 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:04:09 ; Search time 59.1176 Seconds
(without alignments)
116.010 Million cell updates/sec

Title: US-10-749-522-8
Perfect score: 85
Sequence: 1 VHEPHEFRHVALNPV 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
1	85	100.0	15	4	AAB47110	Aab47110 Epitope #
2	85	100.0	15	6	AAO16068	Aao16068 Neurologi
3	85	100.0	15	8	ADJ88115	Adj88115 fd phage
4	85	100.0	15	8	ADK52265	Adk52265 Amyloid b
5	46	54.1	54	4	AAU66289	Aau66289 Propionib
6	46	54.1	54	6	ABM62808	Abm62808 Propionib
7	46	54.1	101	4	AAU50750	Aau50750 Propionib

8	46	54.1	101	6	ABM47269	Abm47269	Propionib
9	46	54.1	446	7	ABM89892	Abm89892	Rice abio
10	45	52.9	12	8	ADQ15529	Adq15529	Targeting
11	45	52.9	12	8	ADQ15532	Adq15532	Targeting
12	45	52.9	12	8	ADQ15528	Adq15528	Targeting
13	45	52.9	267	4	ABG24178	Abg24178	Novel hum
14	45	52.9	443	7	ABO63729	Abo63729	Klebsiell
15	44.5	52.4	917	8	ADO62489	Ado62489	Transcrip
16	44.5	52.4	995	10	AEF11503	Aef11503	Rice meth
17	44	51.8	804	7	ABO72930	Abo72930	Pseudomon
18	43	50.6	322	9	AED14591	Aed14591	VSM-relat
19	43	50.6	543	6	ABU34884	Abu34884	Protein e
20	43	50.6	583	6	ABU33887	Abu33887	Protein e
21	43	50.6	586	6	ABU36674	Abu36674	Protein e
22	43	50.6	1148	8	ADI45347	Adi45347	Rice isop
23	42	49.4	88	5	ABB98895	Abb98895	ATP/GTP c
24	42	49.4	94	4	AAM94427	Aam94427	Human rep
25	42	49.4	94	4	ABB10765	Abb10765	Human ova
26	42	49.4	260	2	AAY50353	Aay50353	Human LOB
27	42	49.4	285	8	ADY23802	Ady23802	Plant ful
28	42	49.4	456	7	ABM88806	Abm88806	Rice abio
29	42	49.4	483	2	AAY50355	Aay50355	Human LOB
30	42	49.4	617	7	ADL22707	Adl22707	Human dis
31	42	49.4	634	9	AEC38987	Aec38987	Bacillus
32	42	49.4	634	9	AEC38979	Aec38979	Bacillus
33	42	49.4	885	5	AAE25384	Aae25384	Human NZM
34	41	48.2	190	8	ADX87906	Adx87906	Plant ful
35	41	48.2	192	9	AED72348	Aed72348	Corynebac
36	41	48.2	205	4	AAB80197	Aab80197	Corynebac
37	41	48.2	205	4	AAB79907	Aab79907	Corynebac
38	41	48.2	224	4	AAB79906	Aab79906	Corynebac
39	41	48.2	224	4	AAB80196	Aab80196	Corynebac
40	41	48.2	239	4	AAG91705	Aag91705	C glutami
41	41	48.2	255	7	ADB65722	Adb65722	Human pro
42	41	48.2	266	4	AAG93150	Aag93150	C glutami
43	41	48.2	294	4	AAU58127	Aau58127	Propionib
44	41	48.2	294	6	ABM54646	Abm54646	Propionib
45	41	48.2	328	3	AAB43187	Aab43187	Human ORF
46	41	48.2	353	7	ABO77357	Abo77357	Pseudomon
47	41	48.2	357	8	ADY14124	Ady14124	Plant ful
48	41	48.2	363	8	ADX73095	Adx73095	Plant ful
49	41	48.2	401	8	ADX87509	Adx87509	Plant ful
50	41	48.2	431	7	ABO67759	Abo67759	Klebsiell
51	41	48.2	462	8	ADX88784	Adx88784	Plant ful
52	41	48.2	573	8	ADX71355	Adx71355	Plant ful
53	41	48.2	579	8	ADX94208	Adx94208	Plant ful
54	41	48.2	623	2	AAW75773	Aaw75773	Amino aci
55	41	48.2	625	4	AAU02044	Aau02044	B. thurin
56	41	48.2	633	2	AAW75775	Aaw75775	Amino aci
57	41	48.2	633	2	AAW75774	Aaw75774	Amino aci
58	41	48.2	764	6	ABU52617	Abu52617	Human NOV
59	41	48.2	801	9	AEA19953	Aea19953	Novel hum
60	41	48.2	804	5	ABB97954	Abb97954	Human pro

Search completed: August 14, 2006, 15:08:44
Job time : 94.1176 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:10:04 ; Search time 27.4118 Seconds
(without alignments)
202.471 Million cell updates/sec

Title: US-10-749-522-7
Perfect score: 38
Sequence: 1 YYEFRH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	38	100.0	376	2	Q8N105_HUMAN	Q8n105 homo sapien
2	38	100.0	516	2	Q7Z5S7_HUMAN	Q7z5s7 homo sapien
3	38	100.0	543	2	Q5D0E6_HUMAN	Q5d0e6 homo sapien
4	38	100.0	543	2	Q86WY1_HUMAN	Q86wyl homo sapien
5	35	92.1	92	2	Q6BG37_PARTE	Q6bg37 paramecium
6	35	92.1	148	2	Q8KNG2_MICEC	Q8kng2 micromonosp
7	35	92.1	154	2	Q84HP9_9ACTO	Q84hp9 micromonosp
8	35	92.1	158	2	Q84HM8_9ACTO	Q84hm8 streptomyce
9	35	92.1	158	2	Q84HN3_9ACTO	Q84hn3 kitasatospo
10	35	92.1	173	2	Q5HV09_CAMJR	Q5hv09 campylobact
11	35	92.1	174	2	Q9PPD6_CAMJE	Q9ppd6 campylobact
12	35	92.1	202	2	Q4N3S3_THEPA	Q4n3s3 theileria p
13	35	92.1	204	2	Q5LR70_SILPO	Q5lr70 silicibacte
14	35	92.1	350	2	Q5FSE4_GLUOX	Q5fse4 gluconobact
15	35	92.1	355	2	Q6TUE0_RAT	Q6tue0 rattus norv

16	35	92.1	362	2	Q8K4B5_MOUSE	Q8k4b5	mus musculu
17	35	92.1	362	2	Q924S2_MOUSE	Q924s2	m 2',5'-oli
18	35	92.1	376	2	Q78ZX0_MOUSE	Q78zx0	mus musculu
19	35	92.1	376	2	Q8JZN0_MOUSE	Q8jzn0	mus musculu
20	35	92.1	376	2	Q8K4E9_MOUSE	Q8k4e9	mus musculu
21	35	92.1	376	2	Q921F0_MOUSE	Q921f0	mus musculu
22	35	92.1	467	2	O96421_DROME	O96421	drosophila
23	35	92.1	467	2	Q9VV72_DROME	Q9vv72	drosophila
24	35	92.1	479	2	Q3U178_MOUSE	Q3u178	mus musculu
25	35	92.1	536	2	Q8BRV6_MOUSE	Q8brv6	mus musculu
26	35	92.1	825	2	Q80VH0_MOUSE	Q80vh0	mus musculu
27	35	92.1	992	2	Q4A0Y6_STAS1	Q4a0y6	staphylococ
28	34	89.5	25	2	Q7R843_PLAYO	Q7r843	plasmodium
29	34	89.5	229	2	Q82KU7_STRAW	Q82ku7	streptomyce
30	34	89.5	315	2	Q8IDQ8_PLAF7	Q8idq8	plasmodium
31	34	89.5	361	2	Q95KH3_MACFA	Q95kh3	macaca fasc
32	34	89.5	409	2	Q2L3B1_BRASY	Q2l3b1	brachypodiu
33	34	89.5	431	2	Q2WB67_MAGSA	Q2wb67	magnetospir
34	34	89.5	469	2	Q8NBC8_HUMAN	Q8nbc8	homo sapien
35	34	89.5	575	2	Q6NT32_HUMAN	Q6nt32	homo sapien
36	34	89.5	654	2	Q36UQ1_MARHY	Q36uq1	marinobacte
37	33	86.8	89	2	Q7R9R9_PLAYO	Q7r9r9	plasmodium
38	33	86.8	186	2	Q2IMQ8_9DELT	Q2imq8	anaeromyxob
39	33	86.8	301	2	Q4DI15_TRYCR	Q4dil5	trypanosoma
40	33	86.8	301	2	Q4DIH0_TRYCR	Q4dih0	trypanosoma
41	33	86.8	305	2	Q386B9_9TRYP	Q386b9	trypanosoma
42	33	86.8	329	2	Q369J6_9GAMM	Q369j6	shewanella
43	33	86.8	359	2	Q3VIU6_9CHLB	Q3viu6	pelodictyon
44	33	86.8	376	2	Q7PNU3_ANOGA	Q7pnu3	anopheles g
45	33	86.8	430	2	Q60424_CRIGR	Q60424	cricetulus
46	33	86.8	483	2	Q4YYH4_PLABE	Q4yyh4	plasmodium
47	33	86.8	580	2	Q60425_CRIGR	Q60425	cricetulus
48	33	86.8	610	2	Q3GE91_9FIRM	Q3ge91	syntrophomo
49	33	86.8	650	2	Q8EP63_OCEIH	Q8ep63	oceanobacil
50	33	86.8	698	2	Q6BGZ2_DEBHA	Q6bgz2	debaryomyce
51	33	86.8	700	2	Q2UQX1_ASPOR	Q2uqx1	aspergillus
52	33	86.8	757	2	Q4SII8_TETNG	Q4sii8	tetraodon n
53	33	86.8	794	2	Q60426_CRIGR	Q60426	cricetulus
54	33	86.8	814	2	Q76KC9_ORYLA	Q76kc9	oryzias lat
55	33	86.8	834	2	Q4S7D2_TETNG	Q4s7d2	tetraodon n
56	33	86.8	927	2	Q6LFU1_PHOPR	Q6lful	photobacter
57	33	86.8	979	2	Q3W9C6_9ACTO	Q3w9c6	frankia sp.
58	33	86.8	1780	2	Q4SQ87_TETNG	Q4sq87	tetraodon n
59	32	84.2	129	2	Q6SA76_9FABA	Q6sa76	vigna radia
60	32	84.2	154	2	Q84HL7_9ACTO	Q84hl7	streptomyce

Search completed: August 14, 2006, 15:17:02

Job time : 67.4118 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:12:05 ; Search time 8 Seconds
 (without alignments)
 72.163 Million cell updates/sec

Title: US-10-749-522-7
 Perfect score: 38
 Sequence: 1 YYEFRH 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
1	35	92.1	174	2	G81349	periplasmic nitrat
2	32	84.2	394	2	T45085	2-oxoisovalerate-f
3	32	84.2	395	2	B75047	probable 2-oxoisov
4	32	84.2	397	2	A71114	probable ferredoxi
5	32	84.2	404	2	C71907	probable type II D
6	32	84.2	425	2	H71167	probable S-adenosy
7	32	84.2	506	2	G86806	lipopolysaccharide
8	32	84.2	600	2	T06775	phosphoinositide-s
9	32	84.2	600	2	T06420	phosphoinositide-s
10	32	84.2	731	2	S29870	DNA-binding protei
11	31	81.6	73	2	A81071	hypothetical prote
12	31	81.6	73	2	E81061	hypothetical prote
13	31	81.6	306	2	G96990	DNA polymerase III

14	31	81.6	338	2	T46981	hypothetical prote
15	31	81.6	338	2	AD0241	probable dehydroge
16	31	81.6	354	2	S15660	(2'-5')oligo(A) sy
17	31	81.6	358	2	S31407	(2'-5')oligo(A) sy
18	31	81.6	367	1	SYMSO1	(2'-5')oligo(A) sy
19	31	81.6	387	2	B82891	ferrichrome transp
20	31	81.6	406	2	S17712	kdgC protein - Erw
21	31	81.6	572	2	S73541	phosphotransferase
22	31	81.6	581	1	S71170	phosphoinositide-s
23	31	81.6	581	2	T50841	phosphoinositide-s
24	31	81.6	634	2	AE2558	hypothetical prote
25	31	81.6	773	2	D86268	Fl3B4.3 protein -
26	31	81.6	1678	2	T35547	hypothetical prote
27	30	78.9	79	2	B36670	cell division cont
28	30	78.9	227	1	QQBEC9	HXLf4 protein prec
29	30	78.9	229	2	B70158	conserved hypothet
30	30	78.9	276	2	F90405	asparinase, probab
31	30	78.9	383	2	JC7507	45K WW domain-cont
32	30	78.9	386	2	S76193	hypothetical prote
33	30	78.9	386	2	JC7508	45K WW domain-cont
34	30	78.9	475	2	G90005	hypothetical prote
35	30	78.9	502	2	AD3563	erythritol-4-phosp
36	30	78.9	532	2	A34329	60K esterase (EC 3
37	30	78.9	557	2	A47162	thiolesterase B (E
38	30	78.9	559	1	JC5408	carboxylesterase (
39	30	78.9	561	2	S47655	carboxylesterase (
40	30	78.9	585	2	T07425	phosphoinositide-s
41	30	78.9	590	2	H70130	oligoendopeptidase
42	30	78.9	605	2	T50842	phospholipase C2 [
43	30	78.9	643	2	H83635	conserved hypothet
44	30	78.9	723	2	I39066	N-methyl-D-asparta
45	30	78.9	726	2	G83310	conserved hypothet
46	30	78.9	741	2	D83633	conserved hypothet
47	30	78.9	872	2	T41147	hypothetical prote
48	30	78.9	1170	2	S30010	probable finger pr
49	30	78.9	1482	2	I49704	glutamate receptor
50	30	78.9	1482	2	B43274	N-methyl-D-asparta
51	30	78.9	1484	2	S52086	N-methyl-D-asparta
52	30	78.9	1498	2	S78102	chitin synthase (E
53	30	78.9	2287	2	T21312	hypothetical prote
54	29	76.3	98	2	A82648	hypothetical prote
55	29	76.3	174	2	D83692	hypothetical prote
56	29	76.3	175	2	C90631	hypothetical prote
57	29	76.3	187	2	B83695	hypothetical prote
58	29	76.3	193	2	G83901	hypothetical prote
59	29	76.3	207	2	C85482	hypothetical prote
60	29	76.3	343	2	AE1146	hypothetical prote

Search completed: August 14, 2006, 15:17:25

Job time : 21 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:20:06 ; Search time 7.17647 Seconds
(without alignments)
56.277 Million cell updates/sec

Title: US-10-749-522-7
Perfect score: 38
Sequence: 1 YYEFRH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*
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2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	34	89.5	413	7	US-11-056-355B-13110 Sequence 13110, A
2	34	89.5	435	7	US-11-056-355B-13109 Sequence 13109, A
3	34	89.5	463	7	US-11-056-355B-13108 Sequence 13108, A
4	32	84.2	186	6	US-10-953-349-22292 Sequence 22292, A
5	32	84.2	191	6	US-10-953-349-22291 Sequence 22291, A
6	32	84.2	225	6	US-10-953-349-28105 Sequence 28105, A
7	32	84.2	233	6	US-10-953-349-28104 Sequence 28104, A
8	32	84.2	275	6	US-10-953-349-28103 Sequence 28103, A
9	32	84.2	314	6	US-10-953-349-22290 Sequence 22290, A

10	32	84.2	894	7	US-11-330-403-18595	Sequence 18595, A
11	30	78.9	79	7	US-11-300-928-55	Sequence 55, Appl
12	30	78.9	86	6	US-10-953-349-22177	Sequence 22177, A
13	30	78.9	86	7	US-11-056-355B-57258	Sequence 57258, A
14	30	78.9	127	6	US-10-953-349-22176	Sequence 22176, A
15	30	78.9	127	7	US-11-056-355B-57257	Sequence 57257, A
16	30	78.9	170	6	US-10-449-902-48648	Sequence 48648, A
17	30	78.9	173	6	US-10-953-349-22175	Sequence 22175, A
18	30	78.9	173	7	US-11-056-355B-57256	Sequence 57256, A
19	30	78.9	446	6	US-10-449-902-42897	Sequence 42897, A
20	30	78.9	466	7	US-11-056-355B-38733	Sequence 38733, A
21	30	78.9	475	7	US-11-330-403-7676	Sequence 7676, Ap
22	30	78.9	481	6	US-10-471-571A-2194	Sequence 2194, Ap
23	30	78.9	486	7	US-11-056-355B-38732	Sequence 38732, A
24	30	78.9	491	7	US-11-056-355B-68168	Sequence 68168, A
25	30	78.9	493	7	US-11-056-355B-68167	Sequence 68167, A
26	30	78.9	501	6	US-10-449-902-45549	Sequence 45549, A
27	30	78.9	511	7	US-11-056-355B-68166	Sequence 68166, A
28	30	78.9	542	7	US-11-227-614-2	Sequence 2, Appli
29	30	78.9	542	7	US-11-227-614-4	Sequence 4, Appli
30	30	78.9	1480	7	US-11-339-440-10	Sequence 10, Appl
31	30	78.9	1480	7	US-11-339-452-10	Sequence 10, Appl
32	29	76.3	458	6	US-10-539-228-568	Sequence 568, App
33	29	76.3	764	7	US-11-330-403-12843	Sequence 12843, A
34	29	76.3	10625	7	US-11-330-403-1837	Sequence 1837, Ap
35	28	73.7	87	7	US-11-056-355B-7885	Sequence 7885, Ap
36	28	73.7	87	7	US-11-056-355B-11876	Sequence 11876, A
37	28	73.7	128	7	US-11-056-355B-7884	Sequence 7884, Ap
38	28	73.7	128	7	US-11-056-355B-11875	Sequence 11875, A
39	28	73.7	179	6	US-10-953-349-2300	Sequence 2300, Ap
40	28	73.7	179	7	US-11-056-355B-40233	Sequence 40233, A
41	28	73.7	179	7	US-11-056-355B-103778	Sequence 103778,
42	28	73.7	179	7	US-11-056-355B-115017	Sequence 115017,
43	28	73.7	209	6	US-10-953-349-2299	Sequence 2299, Ap
44	28	73.7	209	7	US-11-056-355B-40232	Sequence 40232, A
45	28	73.7	209	7	US-11-056-355B-103777	Sequence 103777,
46	28	73.7	209	7	US-11-056-355B-115016	Sequence 115016,
47	28	73.7	216	7	US-11-056-355B-103776	Sequence 103776,
48	28	73.7	216	7	US-11-056-355B-115015	Sequence 115015,
49	28	73.7	222	6	US-10-449-902-45603	Sequence 45603, A
50	28	73.7	251	6	US-10-449-902-42492	Sequence 42492, A
51	28	73.7	265	6	US-10-471-571A-1016	Sequence 1016, Ap
52	28	73.7	353	6	US-10-471-571A-176	Sequence 176, App
53	28	73.7	362	6	US-10-449-902-37167	Sequence 37167, A
54	28	73.7	492	6	US-10-449-902-51390	Sequence 51390, A
55	28	73.7	545	6	US-10-449-902-50416	Sequence 50416, A
56	28	73.7	674	7	US-11-056-355B-90660	Sequence 90660, A
57	28	73.7	674	7	US-11-056-355B-94416	Sequence 94416, A
58	28	73.7	674	7	US-11-330-403-273	Sequence 273, App
59	28	73.7	779	6	US-10-449-902-53491	Sequence 53491, A
60	28	73.7	997	6	US-10-449-902-41237	Sequence 41237, A

Search completed: August 14, 2006, 15:25:09

Job time : 10.4265 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:19:11 ; Search time 29.7647 Seconds
(without alignments)
93.375 Million cell updates/sec

Title: US-10-749-522-7
Perfect score: 38
Sequence: 1 YYEFRH 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
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2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	38	100.0	6	3	US-09-808-037-7	Sequence 7, Appli	
2	38	100.0	6	4	US-10-162-889-7	Sequence 7, Appli	
3	38	100.0	6	4	US-10-384-788-7	Sequence 7, Appli	
4	38	100.0	6	4	US-10-618-856-7	Sequence 7, Appli	
5	38	100.0	6	4	US-10-622-087-90	Sequence 90, Appli	
6	38	100.0	6	5	US-10-749-522-7	Sequence 7, Appli	
7	38	100.0	6	6	US-11-073-526-7	Sequence 7, Appli	
8	38	100.0	8	5	US-10-481-642-1	Sequence 1, Appli	
9	38	100.0	376	4	US-10-104-047-3484	Sequence 3484, Ap	
10	38	100.0	376	4	US-10-104-047-3532	Sequence 3532, Ap	
11	38	100.0	376	6	US-11-072-512-3484	Sequence 3484, Ap	

12	38	100.0	376	6	US-11-072-512-3532	Sequence 3532, Ap
13	38	100.0	516	4	US-10-144-194A-46	Sequence 46, Appl
14	38	100.0	516	5	US-10-491-566-46	Sequence 46, Appl
15	38	100.0	538	4	US-10-144-194A-48	Sequence 48, Appl
16	38	100.0	538	5	US-10-491-566-48	Sequence 48, Appl
17	38	100.0	543	4	US-10-144-194A-44	Sequence 44, Appl
18	38	100.0	543	5	US-10-491-566-44	Sequence 44, Appl
19	38	100.0	585	4	US-10-144-194A-50	Sequence 50, Appl
20	38	100.0	585	5	US-10-491-566-50	Sequence 50, Appl
21	35	92.1	148	4	US-10-152-886-15	Sequence 15, Appl
22	35	92.1	148	6	US-11-053-576-15	Sequence 15, Appl
23	35	92.1	148	6	US-11-053-052-15	Sequence 15, Appl
24	35	92.1	154	4	US-10-152-886-65	Sequence 65, Appl
25	35	92.1	154	6	US-11-053-576-65	Sequence 65, Appl
26	35	92.1	154	6	US-11-053-052-65	Sequence 65, Appl
27	35	92.1	158	4	US-10-152-886-55	Sequence 55, Appl
28	35	92.1	158	6	US-11-053-576-55	Sequence 55, Appl
29	35	92.1	158	6	US-11-053-052-55	Sequence 55, Appl
30	35	92.1	362	4	US-10-439-741-17	Sequence 17, Appl
31	35	92.1	362	6	US-11-012-762-30	Sequence 30, Appl
32	35	92.1	362	6	US-11-012-762-32	Sequence 32, Appl
33	35	92.1	376	4	US-10-439-741-14	Sequence 14, Appl
34	35	92.1	376	6	US-11-012-762-10	Sequence 10, Appl
35	35	92.1	376	6	US-11-012-762-16	Sequence 16, Appl
36	35	92.1	376	6	US-11-012-762-18	Sequence 18, Appl
37	35	92.1	376	6	US-11-012-762-40	Sequence 40, Appl
38	34	89.5	49	3	US-09-864-761-36376	Sequence 36376, A
39	34	89.5	174	4	US-10-767-701-39352	Sequence 39352, A
40	34	89.5	190	4	US-10-425-115-277065	Sequence 277065,
41	34	89.5	229	4	US-10-156-761-9803	Sequence 9803, Ap
42	34	89.5	273	4	US-10-767-701-44740	Sequence 44740, A
43	34	89.5	356	4	US-10-451-168-93	Sequence 93, Appl
44	34	89.5	356	5	US-10-980-387-93	Sequence 93, Appl
45	34	89.5	402	4	US-10-425-114-63108	Sequence 63108, A
46	34	89.5	433	4	US-10-425-115-277059	Sequence 277059,
47	34	89.5	433	6	US-11-087-099-4413	Sequence 4413, Ap
48	34	89.5	435	4	US-10-425-115-265195	Sequence 265195,
49	34	89.5	435	6	US-11-087-099-10693	Sequence 10693, A
50	34	89.5	453	4	US-10-425-115-277063	Sequence 277063,
51	34	89.5	453	4	US-10-425-115-277066	Sequence 277066,
52	34	89.5	453	6	US-11-087-099-4049	Sequence 4049, Ap
53	34	89.5	453	6	US-11-087-099-4060	Sequence 4060, Ap
54	34	89.5	457	6	US-11-087-099-4938	Sequence 4938, Ap
55	34	89.5	469	4	US-10-104-047-2219	Sequence 2219, Ap
56	34	89.5	469	6	US-11-072-512-2219	Sequence 2219, Ap
57	34	89.5	490	4	US-10-425-114-65418	Sequence 65418, A
58	34	89.5	507	4	US-10-425-114-66367	Sequence 66367, A
59	34	89.5	520	4	US-10-425-114-65206	Sequence 65206, A
60	34	89.5	575	4	US-10-451-168-91	Sequence 91, Appl

Search completed: August 14, 2006, 15:24:49

Job time : 46.7647 secs

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OM protein - protein search, using sw_model

Run on: August 14, 2006, 15:15:15 ; Search time 13.7647 Seconds
 (without alignments)
 38.154 Million cell updates/sec

Title: US-10-749-522-7
 Perfect score: 38
 Sequence: 1 YYEFRH 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Issued_Patents_AA:*
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 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	38	100.0	6	2	US-09-830-954A-7	Sequence 7, Appli
2	38	100.0	376	2	US-10-104-047-3484	Sequence 3484, Ap
3	38	100.0	376	2	US-10-104-047-3532	Sequence 3532, Ap
4	35	92.1	148	2	US-10-152-886-15	Sequence 15, Appl
5	35	92.1	154	2	US-10-152-886-65	Sequence 65, Appl
6	35	92.1	158	2	US-10-152-886-55	Sequence 55, Appl
7	34	89.5	469	2	US-10-104-047-2219	Sequence 2219, Ap
8	34	89.5	581	2	US-10-023-515-2,	Sequence 2, Appli
9	34	89.5	581	3	US-10-114-270-196	Sequence 196, App
10	33	86.8	94	2	US-09-902-540-10664	Sequence 10664, A

11	33	86.8	636	2	US-09-248-796A-14866	Sequence 14866, A
12	33	86.8	1180	2	US-09-543-681A-6436	Sequence 6436, Ap
13	32	84.2	88	2	US-09-270-767-33601	Sequence 33601, A
14	32	84.2	88	2	US-09-270-767-48818	Sequence 48818, A
15	32	84.2	154	2	US-10-152-886-85	Sequence 85, Appl
16	32	84.2	165	2	US-10-152-886-95	Sequence 95, Appl
17	32	84.2	502	1	US-08-960-022-10	Sequence 10, Appl
18	32	84.2	577	2	US-09-543-681A-8225	Sequence 8225, Ap
19	32	84.2	899	2	US-09-107-532A-4503	Sequence 4503, Ap
20	31	81.6	147	2	US-09-270-767-37924	Sequence 37924, A
21	31	81.6	147	2	US-09-270-767-53141	Sequence 53141, A
22	31	81.6	152	2	US-10-152-886-25	Sequence 25, Appl
23	31	81.6	153	2	US-10-152-886-35	Sequence 35, Appl
24	31	81.6	157	2	US-10-152-886-5	Sequence 5, Appli
25	31	81.6	162	2	US-10-152-886-3	Sequence 3, Appli
26	31	81.6	324	2	US-09-248-796A-20599	Sequence 20599, A
27	31	81.6	2175	2	US-09-693-205A-8	Sequence 8, Appli
28	31	81.6	3829	2	US-09-693-205A-2	Sequence 2, Appli
29	31	81.6	3829	2	US-09-693-205A-16	Sequence 16, Appl
30	31	81.6	3830	2	US-09-693-205A-4	Sequence 4, Appli
31	30	78.9	79	2	US-09-917-254-64	Sequence 64, Appl
32	30	78.9	110	2	US-09-949-016-9743	Sequence 9743, Ap
33	30	78.9	121	2	US-09-107-532A-5275	Sequence 5275, Ap
34	30	78.9	171	2	US-09-134-001C-5527	Sequence 5527, Ap
35	30	78.9	422	2	US-09-489-039A-12443	Sequence 12443, A
36	30	78.9	425	2	US-10-272-490-84	Sequence 84, Appl
37	30	78.9	449	2	US-10-272-490-18	Sequence 18, Appl
38	30	78.9	449	2	US-10-214-473-18	Sequence 18, Appl
39	30	78.9	457	2	US-09-902-540-11961	Sequence 11961, A
40	30	78.9	466	2	US-09-934-066-2	Sequence 2, Appli
41	30	78.9	488	2	US-09-134-001C-4246	Sequence 4246, Ap
42	30	78.9	542	3	US-10-233-933A-2	Sequence 2, Appli
43	30	78.9	542	3	US-10-233-933A-4	Sequence 4, Appli
44	30	78.9	559	2	US-09-595-682B-28	Sequence 28, Appl
45	30	78.9	559	2	US-09-949-016-6426	Sequence 6426, Ap
46	30	78.9	559	2	US-10-019-219-7	Sequence 7, Appli
47	30	78.9	559	3	US-09-622-568A-28	Sequence 28, Appl
48	30	78.9	571	2	US-10-036-041-23	Sequence 23, Appl
49	30	78.9	577	2	US-09-949-016-9670	Sequence 9670, Ap
50	30	78.9	650	2	US-09-252-991A-17330	Sequence 17330, A
51	30	78.9	749	2	US-09-252-991A-17331	Sequence 17331, A
52	30	78.9	779	2	US-09-252-991A-31290	Sequence 31290, A
53	30	78.9	1347	2	US-09-949-016-9603	Sequence 9603, Ap
54	30	78.9	1456	1	US-08-026-138E-8	Sequence 8, Appli
55	30	78.9	1480	2	US-09-922-011-10	Sequence 10, Appl
56	30	78.9	1482	1	US-08-026-138E-2	Sequence 2, Appli
57	30	78.9	1484	1	US-08-231-193A-56	Sequence 56, Appl
58	30	78.9	1484	1	US-08-486-273A-56	Sequence 56, Appl
59	30	78.9	1484	2	US-08-940-086A-56	Sequence 56, Appl
60	30	78.9	1484	2	US-08-940-035A-56	Sequence 56, Appl

Search completed: August 14, 2006, 15:18:54

Job time : 22.7647 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:04:09 ; Search time 23.6471 Seconds
 (without alignments)
 116.010 Million cell updates/sec

Title: US-10-749-522-7
 Perfect score: 38
 Sequence: 1 YYEFRH 6

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
1	38	100.0	6	4	AAB47109	Aab47109 Epitope #
2	38	100.0	6	6	AAO16067	Aao16067 Neurologi
3	38	100.0	6	8	ADJ88114	Adj88114 fd phage
4	38	100.0	6	8	ADK52266	Adk52266 Amyloid b
5	38	100.0	8	6	ABP70740	Abp70740 Antigenic
6	38	100.0	12	6	ABP70747	Abp70747 Antigenic
7	38	100.0	238	4	AAU23469	Aau23469 Novel hum

8	38	100.0	376	7	ADB65378	Adb65378	Human pro
9	38	100.0	376	7	ADB65330	Adb65330	Human pro
10	38	100.0	516	6	ABR58300	Abr58300	BCU0730B
11	38	100.0	538	6	ABR58301	Abr58301	BCU0730C
12	38	100.0	543	6	ABR58299	Abr58299	BCU0730A
13	38	100.0	585	6	ABR58302	Abr58302	BCU0730D
14	35	92.1	148	5	ABG97423	Abg97423	M. echino
15	35	92.1	148	9	AEB12619	Aeb12619	Thioester
16	35	92.1	148	9	AEC10212	Aec10212	M. echino
17	35	92.1	154	5	ABG97448	Abg97448	M. megalo
18	35	92.1	154	9	AEB12669	Aeb12669	Thioester
19	35	92.1	154	9	AEC10262	Aec10262	Micromono
20	35	92.1	158	5	ABG97443	Abg97443	Kitasatos
21	35	92.1	158	9	AEB12659	Aeb12659	Thioester
22	35	92.1	158	9	AEC10252	Aec10252	Kitasatos
23	35	92.1	362	8	ADJ34669	Adj34669	2'-5' oly
24	35	92.1	362	8	ADJ34668	Adj34668	Mouse 2'-
25	35	92.1	362	8	ADI32343	Adi32343	Mouse OAS
26	35	92.1	376	8	ADJ34673	Adj34673	Mouse 2'-
27	35	92.1	376	8	ADJ34661	Adj34661	Mouse BRV
28	35	92.1	376	8	ADJ34658	Adj34658	Mouse 2'-
29	35	92.1	376	8	ADJ34662	Adj34662	Mouse MOL
30	35	92.1	376	8	ADI32340	Adi32340	Mouse OAS
31	34	89.5	49	4	AAM16665	Aam16665	Peptide #
32	34	89.5	49	4	ABB35649	Abb35649	Peptide #
33	34	89.5	49	4	AAM29149	Aam29149	Peptide #
34	34	89.5	49	4	ABB30482	Abb30482	Peptide #
35	34	89.5	49	4	ABB21078	Abb21078	Protein #
36	34	89.5	49	4	AAM68842	Aam68842	Human bon
37	34	89.5	49	4	AAM56465	Aam56465	Human bra
38	34	89.5	49	4	ABG50502	Abg50502	Human liv
39	34	89.5	49	4	AAM04381	Aam04381	Peptide #
40	34	89.5	49	5	ABG38423	Abg38423	Human pep
41	34	89.5	224	7	ADC55524	Adc55524	Human car
42	34	89.5	356	5	ABP61006	Abp61006	Novel hum
43	34	89.5	402	8	ADY07293	Ady07293	Plant ful
44	34	89.5	469	7	ADB64065	Adb64065	Human pro
45	34	89.5	490	8	ADY09603	Ady09603	Plant ful
46	34	89.5	507	8	ADY10552	Ady10552	Plant ful
47	34	89.5	520	8	ADY09391	Ady09391	Plant ful
48	34	89.5	575	5	ABP61004	Abp61004	Novel hum
49	34	89.5	581	5	ABP61005	Abp61005	Novel hum
50	34	89.5	581	5	ABB79537	Abb79537	Human car
51	34	89.5	581	6	ABU54639	Abu54639	Human NOV
52	34	89.5	581	8	ADQ89094	Adq89094	Human uro
53	34	89.5	618	5	ADR19663	Adr19663	Human dru
54	34	89.5	642	5	AAE25025	Aae25025	Human dru
55	34	89.5	642	8	ABM84114	Abm84114	Human dia
56	33	86.8	10	6	ABP70743	Abp70743	Antigenic
57	33	86.8	14	6	ABP70748	Abp70748	Antigenic
58	33	86.8	94	9	ABM91465	Abm91465	M. xanthu
59	33	86.8	1180	7	ADF06151	Adf06151	Bacterial
60	32	84.2	154	5	ABG97458	Abg97458	S. kaniha
61	32	84.2	154	9	AEB12689	Aeb12689	Thioester
62	32	84.2	154	9	AEC10282	Aec10282	Streptomy
63	32	84.2	165	5	ABG97463	Abg97463	S. citric
64	32	84.2	165	9	AEB12699	Aeb12699	Thioester

65	32	84.2	165	9	AEC10292	Aec10292	Streptomy
66	32	84.2	379	8	ADX68618	Adx68618	Plant ful
67	32	84.2	395	4	AAB96540	Aab96540	Putative
68	32	84.2	398	8	ADN47159	Adn47159	Thermococ
69	32	84.2	425	8	ADS41882	Ads41882	Bacterial
70	32	84.2	425	8	ADN18592	Adn18592	Bacterial
71	32	84.2	427	8	ADX88777	Adx88777	Plant ful
72	32	84.2	502	2	AAW80398	Aaw80398	A secrete
73	32	84.2	506	5	ABB54798	Abb54798	Lactococc
74	32	84.2	532	8	ADN47587	Adn47587	Thermococ
75	32	84.2	577	7	ADF07940	Adf07940	Bacterial
76	32	84.2	609	8	ADY04744	Ady04744	Plant ful
77	32	84.2	616	7	ADC32948	Adc32948	Human nov
78	32	84.2	616	7	ADF60299	Adf60299	Human con
79	32	84.2	666	4	ABB66873	Abb66873	Drosophil
80	32	84.2	666	4	ABB58867	Abb58867	Drosophil
81	32	84.2	731	7	ADK63252	Adk63252	Disease t
82	32	84.2	899	7	ADC94876	Adc94876	E. faeciu
83	31	81.6	6	8	ADQ82436	Adq82436	N-termina
84	31	81.6	6	10	AEF40969	Aef40969	N-termina
85	31	81.6	6	10	AEF40938	Aef40938	N-termina
86	31	81.6	7	10	AEF40929	Aef40929	N-termina
87	31	81.6	124	4	AAO05817	Aao05817	Human pol
88	31	81.6	152	5	ABG97428	Abg97428	S. ghanae
89	31	81.6	152	9	AEB12629	Aeb12629	Thioester
90	31	81.6	152	9	AEC10222	Aec10222	Streptomy
91	31	81.6	153	5	ABG97433	Abg97433	S. carzin
92	31	81.6	153	9	AEB12639	Aeb12639	Thioester
93	31	81.6	153	9	AEC10232	Aec10232	S. carzin
94	31	81.6	157	5	ABG97418	Abg97418	S. macrom
95	31	81.6	157	9	AEB12609	Aeb12609	Thioester
96	31	81.6	157	9	AEC10202	Aec10202	Streptomy
97	31	81.6	162	5	ABG97417	Abg97417	S. macrom
98	31	81.6	162	9	AEB12607	Aeb12607	Thioester
99	31	81.6	162	9	AEC10200	Aec10200	Streptomy
100	31	81.6	173	3	AAG25437	Aag25437	Arabidops

Search completed: August 14, 2006, 15:09:51
Job time : 55.6471 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:10:04 ; Search time 68.5294 Seconds
 (without alignments)
 202.471 Million cell updates/sec

Title: US-10-749-522-22
 Perfect score: 84
 Sequence: 1 STEFRHQTTPLHPNS 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : UniProt_7.2:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	47	56.0	219	2		Q7SHR7_NEUCR	Q7shr7 neurospora
2	46.5	55.4	3298	2		Q9VB11_DROME	Q9vb11 drosophila
3	46	54.8	169	2		Q59V02_CANAL	Q59v02 candida alb
4	45	53.6	126	2		Q6R9H1_MAIZE	Q6r9h1 zea mays (m
5	45	53.6	640	2		Q7RGH6_PLAYO	Q7rgh6 plasmodium
6	44	52.4	302	2		Q5TQQ5_ANOGA	Q5tqq5 anopheles g
7	44	52.4	308	2		Q5TX76_ANOGA	Q5tx76 anopheles g
8	44	52.4	505	2		Q6ZN07_HUMAN	Q6zn07 homo sapien
9	44	52.4	609	1		GLMS_IDILO	Q5qzh5 i glucosami
10	44	52.4	678	2		Q2UES9_ASPOR	Q2ues9 aspergillus
11	44	52.4	691	2		Q43MD7_SOLUS	Q43md7 solibacter
12	44	52.4	2423	2		Q5CQJ6_CRYPV	Q5cqj6 cryptospori
13	43.5	51.8	304	1		Y245_SYNY3	P72702 synechocyst
14	43.5	51.8	681	1		PRZ1_SCHPO	Q09838 schizosacch
15	43	51.2	119	2		Q3FX29_9BURK	Q3fx29 rhodoferax

16	43	51.2	297	2	Q5LY65_STRT1	Q5ly65 streptococc
17	43	51.2	297	2	Q5M2S0_STRT2	Q5m2s0 streptococc
18	43	51.2	394	2	Q3BNS1_XANC5	Q3bns1 xanthomonas
19	43	51.2	523	2	Q3E2F3_CHLAU	Q3e2f3 chloroflexu
20	43	51.2	610	2	Q3CSC7_ALTAT	Q3csc7 pseudoalter
21	43	51.2	901	2	Q7RWJ4_NEUCR	Q7rwj4 neurospora
22	43	51.2	906	2	Q45BS1_9BURK	Q45bs1 burkholderi
23	43	51.2	906	2	Q4LKD0_9BURK	Q4lkd0 burkholderi
24	43	51.2	1323	2	Q4XZK4_PLACH	Q4xzk4 plasmodium
25	43	51.2	1896	2	Q4QJ26_LEIMA	Q4qj26 leishmania
26	43	51.2	4427	2	Q7X0P4_LACFE	Q7x0p4 lactobacill
27	42.5	50.6	2408	2	Q9V549_DROME	Q9v549 drosophila
28	42	50.0	55	2	Q3L8S5_SACKO	Q3l8s5 saccoglossu
29	42	50.0	195	2	Q5SW35_MOUSE	Q5sw35 mus musculu
30	42	50.0	208	2	Q3PWN9_NITHA	Q3pwn9 nitrobacter
31	42	50.0	255	2	Q3QVC4_9RHOB	Q3qvc4 silicibacte
32	42	50.0	271	2	Q4AHQ2_9CHLB	Q4ahq2 chlorobium
33	42	50.0	310	2	Q2T100_BURTH	Q2t100 burkholderi
34	42	50.0	329	2	Q2PRK3_BRARE	Q2prk3 brachydanio
35	42	50.0	475	1	UAP1_SCHPO	O94617 schizosacch
36	42	50.0	596	2	Q3TZN3_MOUSE	Q3tzn3 mus musculu
37	42	50.0	657	1	ACSA_CAMJE	Q9pmd2 campylobact
38	42	50.0	657	2	Q4HDX0_CAMCO	Q4hdx0 campylobact
39	42	50.0	657	2	Q5HSP9_CAMJR	Q5hsp9 campylobact
40	42	50.0	678	2	Q7QUM5_GIALA	Q7qum5 giardia lam
41	42	50.0	893	2	Q5SW34_MOUSE	Q5sw34 mus musculu
42	42	50.0	903	2	Q3TK98_MOUSE	Q3tk98 mus musculu
43	42	50.0	907	2	Q5SW33_MOUSE	Q5sw33 mus musculu
44	42	50.0	914	1	ZFP62_MOUSE	Q8c827 mus musculu
45	42	50.0	914	2	Q3U3H0_MOUSE	Q3u3h0 mus musculu
46	42	50.0	1182	2	Q4N9F0_THEPA	Q4n9f0 theileria p
47	42	50.0	1512	2	Q7XPJ2_ORYSA	Q7xpj2 oryza sativ
48	42	50.0	1625	2	Q4SZD8_TETNG	Q4szd8 tetraodon n
49	42	50.0	7059	1	R1AB_CVBQ	Q8v6w7 b replicase
50	42	50.0	7094	1	R1AB_CVBEN	Q91a29 b replicase
51	42	50.0	7094	1	R1AB_CVBLU	Q8v439 b replicase
52	42	50.0	7094	1	R1AB_CVBM	Q66198 b replicase
53	42	50.0	7095	2	Q2QKN6_9CORO	Q2qkn6 porcine hem
54	42	50.0	7095	2	Q4VID8_CVHOC	Q4vid8 human coron
55	42	50.0	7095	2	Q4VIE7_CVHOC	Q4vie7 human coron
56	42	50.0	7095	2	Q696Q1_CVHOC	Q696q1 human coron
57	42	50.0	7095	2	Q6TNG2_CVHOC	Q6tng2 human coron
58	41.5	49.4	195	1	DCD_HALMA	Q5vld1 haloarcula
59	41.5	49.4	555	2	Q55ZL9_CRYNE	Q55zl9 cryptococcu
60	41.5	49.4	658	2	Q4WR79_ASPFU	Q4wr79 aspergillus

Search completed: August 14, 2006, 15:16:22

Job time : 107.529 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:12:05 ; Search time 20 Seconds
(without alignments)
72.163 Million cell updates/sec

Title: US-10-749-522-22
Perfect score: 84
Sequence: 1 STEFRHQTTPLHPNS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	43.5	51.8	304	1	S74557	acetylpolyamine am
2	43.5	51.8	681	2	S62490	zinc finger protei
3	42	50.0	475	2	T39359	probable udp-n-ace
4	42	50.0	657	2	G81300	acetate-CoA ligase
5	41.5	49.4	706	2	A82091	exodeoxyribonuclea
6	41	48.8	345	2	D84089	hypothetical prote
7	41	48.8	436	2	S48399	hypothetical prote
8	41	48.8	460	2	T45968	hypothetical prote
9	41	48.8	609	2	JC4258	alpha-fetoprotein
10	40.5	48.2	249	2	AB2039	hypothetical prote
11	40.5	48.2	316	2	G82204	transcription regu
12	40.5	48.2	1391	2	T20642	hypothetical prote
13	40.5	48.2	1397	2	E87998	protein F09C3.1 [i

14	40	47.6	330	2	T31704	hypothetical prote
15	40	47.6	605	2	S16561	glutamine-fructose
16	40	47.6	608	1	S01040	glutamine-fructose
17	40	47.6	608	2	B95322	NodM Glutamine ami
18	40	47.6	746	2	G84605	hypothetical prote
19	39	46.4	339	2	T26328	hypothetical prote
20	39	46.4	482	2	S69580	hypothetical prote
21	39	46.4	523	2	D86284	F9L1.1 protein - A
22	39	46.4	606	2	E87263	hypothetical prote
23	39	46.4	1039	2	T22982	hypothetical prote
24	39	46.4	1076	2	T30842	serine-repeat anti
25	39	46.4	1159	2	B95370	probable adenylate
26	39	46.4	1192	2	H88293	protein F59B10.1 [
27	39	46.4	2626	2	T31099	myosin-RhoGAP prot
28	38.5	45.8	295	2	F69976	conserved hypothet
29	38	45.2	207	2	B71446	hypothetical prote
30	38	45.2	294	2	E69817	hypothetical prote
31	38	45.2	305	2	T52299	squamosa promoter
32	38	45.2	311	1	QQBEC1	HKLF1 protein - hu
33	38	45.2	367	2	G71803	hypothetical prote
34	38	45.2	467	2	G82081	UDP-N-acetylmuramo
35	38	45.2	496	2	S58300	probable excision
36	38	45.2	526	2	S46766	hypothetical prote
37	38	45.2	609	2	AB0500	glutamine-fructose
38	38	45.2	629	2	A30168	homeotic protein L
39	38	45.2	726	2	T51519	cyclic nucleotide-
40	38	45.2	825	2	S62042	probable membrane
41	38	45.2	1802	2	S69703	HKR1 protein precu
42	38	45.2	2140	2	T18543	probable cell-adhe
43	37	44.0	109	2	A83934	hypothetical prote
44	37	44.0	222	2	AE2191	hypothetical prote
45	37	44.0	299	2	AB1776	hypothetical prote
46	37	44.0	338	2	F82358	lysophospholipase
47	37	44.0	351	2	E97187	dTDP-D-glucose 4,6
48	37	44.0	385	2	S49752	homeotic protein Y
49	37	44.0	419	2	H81667	transcription term
50	37	44.0	464	2	A71509	probable transcrip
51	37	44.0	518	1	XYIMHA	homoserine O-acety
52	37	44.0	519	2	H86897	gluconokinase (EC
53	37	44.0	536	2	S40717	hypothetical prote
54	37	44.0	559	2	F96500	hypothetical prote
55	37	44.0	643	2	B71848	probable outer mem
56	37	44.0	710	2	T22360	hypothetical prote
57	37	44.0	748	1	S08680	methylmalonyl-CoA
58	37	44.0	750	1	A59145	methylmalonyl-CoA
59	37	44.0	788	2	S53923	probable membrane
60	37	44.0	863	2	S06017	neuraxin - rat

Search completed: August 14, 2006, 15:17:12

Job time : 35 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:20:06 ; Search time 17.9412 Seconds
 (without alignments)
 56.277 Million cell updates/sec

Title: US-10-749-522-22
 Perfect score: 84.
 Sequence: 1 STEFRHQTTPLHPNS 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	43	51.2	264	7	US-11-317-789A-719	Sequence 719, App
2	42.5	50.6	316	7	US-11-056-355B-55593	Sequence 55593, A
3	42.5	50.6	338	7	US-11-056-355B-55592	Sequence 55592, A
4	42.5	50.6	349	7	US-11-056-355B-55591	Sequence 55591, A
5	42	50.0	315	7	US-11-056-355B-5101	Sequence 5101, Ap
6	42	50.0	635	7	US-11-056-355B-72152	Sequence 72152, A
7	42	50.0	710	7	US-11-056-355B-72151	Sequence 72151, A
8	42	50.0	710	7	US-11-056-355B-86609	Sequence 86609, A
9	41	48.8	308	6	US-10-953-349-26736	Sequence 26736, A

10	40	47.6	170	6	US-10-449-902-41030	Sequence 41030, A
11	40	47.6	258	7	US-11-056-355B-16289	Sequence 16289, A
12	40	47.6	448	7	US-11-174-307B-3428	Sequence 3428, Ap
13	40	47.6	473	7	US-11-056-355B-16288	Sequence 16288, A
14	40	47.6	508	7	US-11-056-355B-16287	Sequence 16287, A
15	39	46.4	575	7	US-11-056-355B-44632	Sequence 44632, A
16	39	46.4	575	7	US-11-056-355B-76951	Sequence 76951, A
17	39	46.4	578	7	US-11-056-355B-44631	Sequence 44631, A
18	39	46.4	578	7	US-11-056-355B-76950	Sequence 76950, A
19	39	46.4	729	7	US-11-121-133-268	Sequence 268, App
20	38.5	45.8	262	6	US-10-449-902-41759	Sequence 41759, A
21	38	45.2	127	6	US-10-953-349-13146	Sequence 13146, A
22	38	45.2	149	6	US-10-953-349-13145	Sequence 13145, A
23	38	45.2	179	6	US-10-953-349-13144	Sequence 13144, A
24	38	45.2	209	6	US-10-953-349-867	Sequence 867, App
25	38	45.2	209	7	US-11-056-355B-28617	Sequence 28617, A
26	38	45.2	209	7	US-11-056-355B-29397	Sequence 29397, A
27	38	45.2	209	7	US-11-056-355B-32207	Sequence 32207, A
28	38	45.2	209	7	US-11-056-355B-32987	Sequence 32987, A
29	38	45.2	209	7	US-11-056-355B-91370	Sequence 91370, A
30	38	45.2	209	7	US-11-056-355B-95126	Sequence 95126, A
31	38	45.2	222	7	US-11-056-355B-16655	Sequence 16655, A
32	38	45.2	249	7	US-11-317-789A-517	Sequence 517, App
33	38	45.2	249	7	US-11-317-789A-518	Sequence 518, App
34	38	45.2	289	6	US-10-953-349-866	Sequence 866, App
35	38	45.2	289	7	US-11-056-355B-28616	Sequence 28616, A
36	38	45.2	289	7	US-11-056-355B-29396	Sequence 29396, A
37	38	45.2	289	7	US-11-056-355B-32206	Sequence 32206, A
38	38	45.2	289	7	US-11-056-355B-32986	Sequence 32986, A
39	38	45.2	289	7	US-11-056-355B-91369	Sequence 91369, A
40	38	45.2	289	7	US-11-056-355B-95125	Sequence 95125, A
41	38	45.2	289	7	US-11-056-355B-108600	Sequence 108600,
42	38	45.2	289	7	US-11-056-355B-119839	Sequence 119839,
43	38	45.2	361	7	US-11-056-355B-91368	Sequence 91368, A
44	38	45.2	361	7	US-11-056-355B-95124	Sequence 95124, A
45	38	45.2	373	6	US-10-953-349-865	Sequence 865, App
46	38	45.2	373	7	US-11-113-081A-2	Sequence 2, Appli
47	38	45.2	373	7	US-11-056-355B-28615	Sequence 28615, A
48	38	45.2	373	7	US-11-056-355B-29395	Sequence 29395, A
49	38	45.2	373	7	US-11-056-355B-32205	Sequence 32205, A
50	38	45.2	373	7	US-11-056-355B-32985	Sequence 32985, A
51	38	45.2	373	7	US-11-056-355B-108599	Sequence 108599,
52	38	45.2	373	7	US-11-056-355B-119838	Sequence 119838,
53	38	45.2	389	7	US-11-056-355B-108598	Sequence 108598,
54	38	45.2	389	7	US-11-056-355B-119837	Sequence 119837,
55	38	45.2	439	6	US-10-953-349-19898	Sequence 19898, A
56	38	45.2	498	7	US-11-056-355B-79485	Sequence 79485, A
57	38	45.2	525	7	US-11-056-355B-79484	Sequence 79484, A
58	38	45.2	2304	6	US-10-540-898-310	Sequence 310, App
59	37.5	44.6	851	6	US-10-540-898-397	Sequence 397, App
60	37	44.0	34	7	US-11-223-610-56	Sequence 56, Appl

Search completed: August 14, 2006, 15:25:06

Job time : 22.1912 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:19:11 ; Search time 74.4118 Seconds
(without alignments)
93.375 Million cell updates/sec

Title: US-10-749-522-22
Perfect score: 84
Sequence: 1 STEFRHQTTPLHPNS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	84	100.0	15	3	US-09-808-037-22	Sequence 22, Appl
2	84	100.0	15	4	US-10-162-889-22	Sequence 22, Appl
3	84	100.0	15	4	US-10-384-788-22	Sequence 22, Appl
4	84	100.0	15	4	US-10-618-856-22	Sequence 22, Appl
5	84	100.0	15	5	US-10-749-522-22	Sequence 22, Appl
6	84	100.0	15	6	US-11-073-526-22	Sequence 22, Appl
7	59	70.2	335	4	US-10-437-963-177702	Sequence 177702,
8	46.5	55.4	126	4	US-10-424-599-236661	Sequence 236661,
9	46	54.8	227	4	US-10-425-114-55911	Sequence 55911, A
10	46	54.8	305	4	US-10-437-963-143406	Sequence 143406,
11	46	54.8	377	4	US-10-424-599-241171	Sequence 241171,

12	45	53.6	81	4	US-10-437-963-124802	Sequence 124802,
13	45	53.6	642	4	US-10-437-963-140313	Sequence 140313,
14	44	52.4	83	4	US-10-437-963-192253	Sequence 192253,
15	44	52.4	180	4	US-10-437-963-111252	Sequence 111252,
16	43.5	51.8	304	6	US-11-087-099-10045	Sequence 10045, A
17	43	51.2	128	4	US-10-425-115-354458	Sequence 354458,
18	43	51.2	626	6	US-11-188-298-22376	Sequence 22376, A
19	43	51.2	901	6	US-11-087-099-1818	Sequence 1818, Ap
20	42.5	50.6	316	6	US-11-096-568A-3300	Sequence 3300, Ap
21	42.5	50.6	338	6	US-11-096-568A-3299	Sequence 3299, Ap
22	42.5	50.6	349	6	US-11-096-568A-3298	Sequence 3298, Ap
23	42.5	50.6	543	4	US-10-425-114-51382	Sequence 51382, A
24	42.5	50.6	570	4	US-10-424-599-156730	Sequence 156730,
25	42	50.0	61	4	US-10-425-115-310263	Sequence 310263,
26	42	50.0	61	4	US-10-425-115-364223	Sequence 364223,
27	42	50.0	85	4	US-10-424-599-143717	Sequence 143717,
28	42	50.0	100	4	US-10-425-115-339083	Sequence 339083,
29	42	50.0	159	4	US-10-437-963-188976	Sequence 188976,
30	42	50.0	577	4	US-10-029-180-48	Sequence 48, Appl
31	42	50.0	577	5	US-10-952-045-48	Sequence 48, Appl
32	42	50.0	635	6	US-11-096-568A-29628	Sequence 29628, A
33	42	50.0	657	4	US-10-282-122A-54608	Sequence 54608, A
34	42	50.0	710	6	US-11-096-568A-29627	Sequence 29627, A
35	42	50.0	1243	4	US-10-437-963-124960	Sequence 124960,
36	42	50.0	1512	4	US-10-437-963-181358	Sequence 181358,
37	41.5	49.4	706	4	US-10-282-122A-77432	Sequence 77432, A
38	41	48.8	60	4	US-10-425-115-296073	Sequence 296073,
39	41	48.8	100	4	US-10-437-963-106615	Sequence 106615,
40	41	48.8	144	4	US-10-424-599-239420	Sequence 239420,
41	41	48.8	247	6	US-11-182-480-57	Sequence 57, Appl
42	41	48.8	247	6	US-11-182-480-58	Sequence 58, Appl
43	41	48.8	247	6	US-11-182-408-57	Sequence 57, Appl
44	41	48.8	247	6	US-11-182-408-58	Sequence 58, Appl
45	41	48.8	295	5	US-10-898-775-4	Sequence 4, Appli
46	41	48.8	295	5	US-10-898-775-5	Sequence 5, Appli
47	41	48.8	295	5	US-10-911-160-4	Sequence 4, Appli
48	41	48.8	295	5	US-10-911-160-5	Sequence 5, Appli
49	41	48.8	295	6	US-11-182-480-4	Sequence 4, Appli
50	41	48.8	295	6	US-11-182-480-5	Sequence 5, Appli
51	41	48.8	295	6	US-11-182-408-4	Sequence 4, Appli
52	41	48.8	295	6	US-11-182-408-5	Sequence 5, Appli
53	41	48.8	1583	4	US-10-437-963-190592	Sequence 190592,
54	40.5	48.2	155	4	US-10-424-599-205115	Sequence 205115,
55	40	47.6	65	4	US-10-425-115-258104	Sequence 258104,
56	40	47.6	112	4	US-10-437-963-147941	Sequence 147941,
57	40	47.6	139	4	US-10-425-115-205443	Sequence 205443,
58	40	47.6	145	5	US-10-450-763-52419	Sequence 52419, A
59	40	47.6	180	4	US-10-424-599-234183	Sequence 234183,
60	40	47.6	186	4	US-10-425-115-255363	Sequence 255363,

Search completed: August 14, 2006, 15:24:32

Job time : 90.4118 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:15:15 ; Search time 34.4118 Seconds
(without alignments)
38.154 Million cell updates/sec

Title: US-10-749-522-22
Perfect score: 84
Sequence: 1 STEFRHQTTPLHPNS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued_Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	84	100.0	15	2	US-09-830-954A-22	Sequence 22, Appl
2	51	60.7	656	2	US-09-902-540-9810	Sequence 9810, Ap
3	46	54.8	192	2	US-09-248-796A-26839	Sequence 26839, A
4	43	51.2	940	2	US-09-328-352-8165	Sequence 8165, Ap
5	42	50.0	577	2	US-10-029-180-48	Sequence 48, Appl
6	42	50.0	708	2	US-09-489-039A-10131	Sequence 10131, A
7	40	47.6	315	2	US-09-248-796A-18003	Sequence 18003, A
8	39.5	47.0	800	2	US-09-949-016-7703	Sequence 7703, Ap
9	39.5	47.0	947	2	US-09-418-780A-1	Sequence 1, Appli
10	39.5	47.0	947	2	US-09-392-714-23	Sequence 23, Appl

11	39	46.4	315	2	US-09-248-796A-23418	Sequence 23418, A
12	39	46.4	317	2	US-09-248-796A-26237	Sequence 26237, A
13	39	46.4	403	2	US-09-270-767-44912	Sequence 44912, A
14	39	46.4	455	2	US-09-270-767-35242	Sequence 35242, A
15	39	46.4	455	2	US-09-270-767-50459	Sequence 50459, A
16	39	46.4	729	1	US-08-971-937-2	Sequence 2, Appli
17	39	46.4	729	1	US-08-812-533-2	Sequence 2, Appli
18	39	46.4	729	2	US-09-771-161A-268	Sequence 268, App
19	39	46.4	749	2	US-09-949-016-10745	Sequence 10745, A
20	38	45.2	103	2	US-09-621-976-6639	Sequence 6639, Ap
21	38	45.2	276	2	US-09-270-767-32903	Sequence 32903, A
22	38	45.2	276	2	US-09-270-767-48120	Sequence 48120, A
23	38	45.2	331	2	US-09-252-991A-24420	Sequence 24420, A
24	38	45.2	345	2	US-09-489-039A-9471	Sequence 9471, Ap
25	38	45.2	395	2	US-09-252-991A-30497	Sequence 30497, A
26	38	45.2	492	2	US-09-710-279-1276	Sequence 1276, Ap
27	38	45.2	503	2	US-09-134-001C-3457	Sequence 3457, Ap
28	38	45.2	1456	2	US-09-949-016-9853	Sequence 9853, Ap
29	38	45.2	1891	1	US-08-804-227C-12	Sequence 12, Appl
30	38	45.2	1891	1	US-08-804-198-6	Sequence 6, Appli
31	37.5	44.6	322	2	US-09-328-352-4547	Sequence 4547, Ap
32	37.5	44.6	515	2	US-09-107-532A-6749	Sequence 6749, Ap
33	37	44.0	62	2	US-09-134-001C-4983	Sequence 4983, Ap
34	37	44.0	77	2	US-09-513-999C-4965	Sequence 4965, Ap
35	37	44.0	150	2	US-09-596-377A-33	Sequence 33, Appl
36	37	44.0	243	2	US-09-248-796A-14531	Sequence 14531, A
37	37	44.0	246	2	US-09-248-796A-18240	Sequence 18240, A
38	37	44.0	252	2	US-09-270-767-44627	Sequence 44627, A
39	37	44.0	335	2	US-09-252-991A-26591	Sequence 26591, A
40	37	44.0	412	2	US-09-902-540-15047	Sequence 15047, A
41	37	44.0	545	2	US-09-134-000C-3545	Sequence 3545, Ap
42	37	44.0	585	2	US-09-107-532A-4126	Sequence 4126, Ap
43	37	44.0	668	2	US-09-252-991A-22794	Sequence 22794, A
44	37	44.0	736	2	US-09-949-016-7488	Sequence 7488, Ap
45	37	44.0	739	2	US-08-510-646B-33	Sequence 33, Appl
46	37	44.0	819	2	US-09-543-681A-7385	Sequence 7385, Ap
47	37	44.0	820	2	US-09-328-352-5766	Sequence 5766, Ap
48	37	44.0	820	2	US-09-489-039A-12169	Sequence 12169, A
49	37	44.0	924	2	US-09-248-796A-18798	Sequence 18798, A
50	37	44.0	1014	2	US-09-492-709A-266	Sequence 266, App
51	37	44.0	1038	2	US-09-215-569B-12	Sequence 12, Appl
52	36.5	43.5	234	2	US-09-270-767-45995	Sequence 45995, A
53	36.5	43.5	303	2	US-09-270-767-45675	Sequence 45675, A
54	36.5	43.5	1085	2	US-09-198-452A-961	Sequence 961, App
55	36.5	43.5	1087	2	US-09-438-185A-893	Sequence 893, App
56	36	42.9	24	2	US-08-838-413A-27	Sequence 27, Appl
57	36	42.9	24	2	US-09-355-581-27	Sequence 27, Appl
58	36	42.9	84	2	US-09-489-847-147	Sequence 147, App
59	36	42.9	109	2	US-09-513-999C-5688	Sequence 5688, Ap
60	36	42.9	124	2	US-09-513-999C-5276	Sequence 5276, Ap

Search completed: August 14, 2006, 15:18:45

Job time : 44.4118 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:04:09 ; Search time 59.1176 Seconds
 (without alignments)
 116.010 Million cell updates/sec

Title: US-10-749-522-22
 Perfect score: 84
 Sequence: 1 STEFRHQTTPLHPNS 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
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 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	84	100.0	15	4	AAB47117	Aab47117 EFRH cont	
2	84	100.0	15	6	AAO16077	Aao16077 Neurologi	
3	84	100.0	15	8	ADJ88128	Adj88128 Anti-aggr	
4	51	60.7	656	9	ABM90611	Abm90611 M. xanthu	
5	46	54.8	227	8	ADX93247	Adx93247 Plant ful	
6	44	52.4	185	5	ABP66058	Abp66058 Bifidobac	
7	44	52.4	505	8	ADQ67682	Adq67682 Novel hum	

8	43	51.2	156	4	ABB15642	Abb15642	Human ner
9	43	51.2	940	6	ADA36878	Ada36878	Acinetoba
10	42.5	50.6	543	8	ADX88718	Adx88718	Plant ful
11	42	50.0	577	5	ABP63107	Abp63107	FLO11 gen
12	42	50.0	657	6	ABU26684	Abu26684	Protein e
13	42	50.0	708	7	ABO63614	Abo63614	Klebsiell
14	42	50.0	7094	8	ABY03145	Aby03145	Bovine co
15	41.5	49.4	706	6	ABU49508	Abu49508	Protein e
16	41.5	49.4	706	8	ADR31327	Adr31327	Aspergill
17	41	48.8	295	8	ADR41617	Adr41617	Lipid acy
18	41	48.8	295	8	ADR41618	Adr41618	Lipid acy
19	41	48.8	295	8	ADR41567	Adr41567	Lipid acy
20	41	48.8	295	8	ADR41568	Adr41568	Lipid acy
21	41	48.8	295	9	AEB44070	Aeb44070	Lipid acy
22	41	48.8	295	9	AEB44069	Aeb44069	Lipid acy
23	41	48.8	295	9	AEB28310	Aeb28310	Glycolipi
24	41	48.8	295	9	AEB28311	Aeb28311	Glycolipi
25	41	48.8	295	10	AEF62807	Aef62807	Lipid acy
26	41	48.8	295	10	AEF62806	Aef62806	Lipid acy
27	40	47.6	50	5	ABP09600	Abp09600	Human ORF
28	40	47.6	77	4	AAO05814	Aao05814	Human pol
29	40	47.6	121	8	ADR09989	Adr09989	Human pro
30	40	47.6	145	4	ABG22060	Abg22060	Novel hum
31	40	47.6	191	8	ADX76729	Adx76729	Plant ful
32	40	47.6	395	7	ADB70108	Adb70108	C. neofor
33	40	47.6	473	4	ABB71149	Abb71149	Drosophil
34	40	47.6	553	6	ABR40771	Abr40771	Glycine m
35	40	47.6	607	8	ADS23171	Ads23171	Bacterial
36	40	47.6	629	8	ADS42606	Ads42606	Bacterial
37	39.5	47.0	124	4	ABG11004	Abg11004	Novel hum
38	39.5	47.0	233	4	ABG03905	Abg03905	Novel hum
39	39.5	47.0	324	9	AED96153	Aed96153	Human C-r
40	39.5	47.0	452	5	AAU79412	Aau79412	Human tra
41	39.5	47.0	528	4	AAB98977	Aab98977	Human PCL
42	39.5	47.0	528	6	ABU03462	Abu03462	Angiogene
43	39.5	47.0	528	8	ADI82178	Adi82178	Human pod
44	39.5	47.0	528	8	ADO44007	Ado44007	Amino aci
45	39.5	47.0	528	8	ADR70488	Adr70488	Human pod
46	39.5	47.0	528	9	ADV41988	Adv41988	Human pod
47	39.5	47.0	528	9	AED96152	Aed96152	Human C-r
48	39.5	47.0	528	9	AED96151	Aed96151	Human C-r
49	39.5	47.0	947	2	AAW81168	Aaw81168	Transcrip
50	39.5	47.0	947	2	AAU07114	Aay07114	WO9904265
51	39.5	47.0	947	8	ADJ96674	Adj96674	Human aty
52	39.5	47.0	947	8	ADJ54137	Adj54137	Human bro
53	39	46.4	26	4	ABG59772	Abg59772	Human liv
54	39	46.4	50	4	AAU48924	Aau48924	Propionib
55	39	46.4	50	6	ABM45443	Abm45443	Propionib
56	39	46.4	56	4	AAU61706	Aau61706	Propionib
57	39	46.4	56	6	ABM58225	Abm58225	Propionib
58	39	46.4	66	5	ABP08718	Abp08718	Human ORF
59	39	46.4	112	4	AAU86535	Aau86535	Novel hum
60	39	46.4	112	7	ADB59869	Adb59869	Connectiv

Search completed: August 14, 2006, 15:09:19

Job time : 94.1176 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:10:04 ; Search time 68.5294 Seconds
(without alignments)
202.471 Million cell updates/sec

Title: US-10-749-522-21
Perfect score: 78
Sequence: 1 DTEFRHSSNNFSAVR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
1	44	56.4	1100	2	Q5KF71	CRYNE	Q5kf71 cryptococcu
2	44	56.4	1127	2	Q55QZ7	CRYNE	Q55qz7 cryptococcu
3	43	55.1	1421	2	Q7QPX0	GIALA	Q7qpx0 giardia lam
4	42	53.8	112	2	Q4AC56	9SPHN	Q4ac56 sphingomona
5	42	53.8	190	2	Q80S36	9VIRU	Q80s36 mayaro viru
6	42	53.8	342	2	Q82DV3	STRAW	Q82dv3 streptomyce
7	42	53.8	394	2	Q4S539	TETNG	Q4s539 tetraodon n
8	42	53.8	530	2	Q61Q18	CAEBR	Q61q18 caenorhabdi
9	42	53.8	628	2	Q22015	CAEEL	Q22015 caenorhabdi
10	42	53.8	1121	2	Q9AKN9	RICMO	Q9akn9 rickettsia
11	42	53.8	2437	2	Q8QZ73	9VIRU	Q8qz73 mayaro viru
12	41	52.6	23	1	IAPP	LEPEU	Q07333 lepus europ
13	41	52.6	67	1	IAPP	RABIT	Q07334 oryctolagus
14	41	52.6	89	1	IAPP	HUMAN	P10997 homo sapien
15	41	52.6	112	2	Q5GRF6	ALCXX	Q5grf6 alcaligenes

16	41	52.6	112	2	Q8RSJ8_9BACT	Q8rsj8 uncultured
17	41	52.6	113	2	P71177_ENTAE	P71177 enterobacte
18	41	52.6	113	2	Q2VLE6_BURCE	Q2vle6 burkholderi
19	41	52.6	113	2	Q56467_9ZZZZ	Q56467 plasmid r75
20	41	52.6	113	2	Q6UP65_RALEJ	Q6up65 ralstonia e
21	41	52.6	113	2	Q76M42_COMAC	Q76m42 comamonas a
22	41	52.6	113	2	Q79BP5_PSESD	Q79bp5 pseudomonas
23	41	52.6	113	2	Q7BHY8_COMTE	Q7bhy8 comamonas t
24	41	52.6	113	2	Q7X3A2_9BACT	Q7x3a2 uncultured
25	41	52.6	113	2	Q3F2F0_9BURK	Q3f2f0 burkholderi
26	41	52.6	113	2	Q4LCG0_9ZZZZ	Q4lcg0 incp-lbeta
27	41	52.6	113	2	Q5W3K4_9ZZZZ	Q5w3k4 plasmid pb3
28	41	52.6	117	2	Q87K58_VIBPA	Q87k58 vibrio para
29	41	52.6	161	2	Q7PB85_RICSI	Q7pb85 rickettsia
30	41	52.6	182	2	Q4UKR0_RICFE	Q4ukr0 rickettsia
31	41	52.6	184	2	Q92IR8_RICCN	Q92ir8 rickettsia
32	41	52.6	323	2	Q4XGF4_PLACH	Q4xgf4 plasmodium
33	41	52.6	363	1	Y2500_AGRT5	P58759 agrobacteri
34	41	52.6	476	2	Q4N593_THEPA	Q4n593 theileria p
35	41	52.6	527	2	Q4PB46_USTMA	Q4pb46 ustilago ma
36	41	52.6	670	2	Q7S6G9_NEUCR	Q7s6g9 neurospora
37	41	52.6	760	2	Q8I8Y0_MANSE	Q8i8y0 manduca sex
38	41	52.6	805	2	Q5A287_CANAL	Q5a287 candida alb
39	41	52.6	808	2	Q5A2D8_CANAL	Q5a2d8 candida alb
40	41	52.6	931	1	STE13_YEAST	P33894 saccharomyc
41	40	51.3	193	2	Q40IL2_EHRCH	Q40il2 ehrlichia c
42	40	51.3	279	2	Q5F759_NEIG1	Q5f759 neisseria g
43	40	51.3	279	2	Q9JT84_NEIMA	Q9jt84 neisseria m
44	40	51.3	279	2	Q9JYA2_NEIMB	Q9jya2 neisseria m
45	40	51.3	285	2	Q70GH8_NEISU	Q70gh8 neisseria s
46	40	51.3	350	2	Q2P7K9_XANOR	Q2p7k9 xanthomonas
47	40	51.3	350	2	Q5H4T4_XANOR	Q5h4t4 xanthomonas
48	40	51.3	411	2	Q965X2_CAEEL	Q965x2 caenorhabdi
49	40	51.3	411	2	Q965X3_CAEEL	Q965x3 caenorhabdi
50	40	51.3	469	2	Q8GUA8_MEDTR	Q8gua8 medicago tr
51	40	51.3	488	2	Q8XUR6_RALSO	Q8xur6 ralstonia s
52	40	51.3	717	2	Q4SR34_TETNG	Q4sr34 tetraodon n
53	40	51.3	720	1	EXO84_KLULA	Q6cnm8 kluyveromyc
54	40	51.3	814	2	O52984_ECOLI	O52984 escherichia
55	40	51.3	834	2	Q92LD3_RHIME	Q92ld3 rhizobium m
56	40	51.3	958	1	K6PF2_YEAST	P16862 saccharomyc
57	40	51.3	1161	2	Q57UJ3_9TRYP	Q57uj3 trypanosoma
58	40	51.3	1517	2	Q59DW9_DROME	Q59dw9 drosophila
59	40	51.3	1517	2	Q6XK18_DROME	Q6xk18 drosophila
60	40	51.3	2645	2	Q6XK19_DROME	Q6xk19 drosophila
61	40	51.3	3044	2	Q63CQ6_BACCZ	Q63cq6 bacillus ce
62	39	50.0	116	1	SPT4H_DROME	Q9tvq5 drosophila
63	39	50.0	193	2	Q07246_YEAST	Q07246 saccharomyc
64	39	50.0	203	2	Q2JE42_9ACTO	Q2je42 frankia sp.
65	39	50.0	229	2	Q3FKW1_9BURK	Q3fkw1 rhodoferax

Search completed: August 14, 2006, 15:14:56

Job time : 120.529 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:12:05 ; Search time 20 Seconds
 (without alignments)
 72.163 Million cell updates/sec

Title: US-10-749-522-21
 Perfect score: 78
 Sequence: 1 DTEFRHSSNNFSAVR 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : PIR_80:*
 1: pir1:*
 2: pir2:*
 3: pir3:*
 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
1	42	53.8	628	2	T24241	hypothetical prote	
2	41	52.6	23	2	I46933	islet amyloid poly	
3	41	52.6	23	2	I46934	islet amyloid poly	
4	41	52.6	89	1	TCHUIA	islet amyloid poly	
5	41	52.6	113	2	T08497	single-strand DNA-	
6	41	52.6	184	2	H97743	hypothetical prote	
7	41	52.6	318	2	AI2883	conserved hypothet	
8	41	52.6	363	2	G97659	hypothetical prote	
9	41	52.6	931	2	A49737	dipeptidyl aminope	
10	40	51.3	279	2	G81054	cytochrome c5 NMB1	
11	40	51.3	279	2	F81821	probable cytochrom	
12	40	51.3	959	1	JQ0017	6-phosphofructokin	
13	39	50.0	193	4	S59326	hypothetical prote	

14	39	50.0	373	2	S52635	1-aminocyclopropan
15	39	50.0	526	2	AH0601	probable membrane
16	39	50.0	582	2	S10099	transcription fact
17	39	50.0	654	2	A34734	transcription fact
18	39	50.0	742	4	C34734	transcription fact
19	39	50.0	825	4	B34734	transcription fact
20	38	48.7	184	2	D71681	hypothetical prote
21	38	48.7	235	2	S69757	hypothetical prote
22	38	48.7	340	2	T21805	hypothetical prote
23	38	48.7	433	2	AC2275	hypothetical prote
24	38	48.7	436	2	A37953	transcription regu
25	38	48.7	638	2	B35816	transcription regu
26	38	48.7	649	1	B37953	transcription regu
27	38	48.7	649	2	A35816	transcription regu
28	38	48.7	835	2	T15177	hypothetical prote
29	38	48.7	1108	2	T17455	translation initia
30	38	48.7	1122	2	A97814	transcription-repa
31	38	48.7	1583	2	S59644	sister chromatid c
32	37.5	48.1	303	2	S71185	splicing factor SF
33	37.5	48.1	303	2	F86158	alternative splici
34	37	47.4	190	2	AH2216	nitrate transport
35	37	47.4	266	2	C84963	extragenic suppres
36	37	47.4	289	2	AH0484	conserved hypothet
37	37	47.4	296	2	T31582	hypothetical prote
38	37	47.4	327	2	T25780	hypothetical prote
39	37	47.4	401	2	T25784	hypothetical prote
40	37	47.4	427	1	S63615	malF protein homol
41	37	47.4	450	2	AF1884	glycolate oxidase
42	37	47.4	484	2	G72395	alpha-L-arabinofur
43	37	47.4	540	2	T47858	hypothetical prote
44	37	47.4	744	2	C90089	hypothetical prote
45	37	47.4	762	2	T14815	hypothetical prote
46	37	47.4	1028	2	G96769	unknown protein F9
47	37	47.4	1092	2	S42798	fibronectin-bindin
48	37	47.4	1117	2	S33851	fibronectin-bindin
49	37	47.4	1218	2	T29915	hypothetical prote
50	37	47.4	2957	2	T33152	hypothetical prote
51	36.5	46.8	411	2	S46800	LAG1 protein - yea
52	36.5	46.8	489	2	C75269	hypothetical prote
53	36	46.2	116	2	S07258	helix-destabilizin
54	36	46.2	201	2	E82695	hypothetical prote
55	36	46.2	230	2	AC0474	conserved hypothet
56	36	46.2	234	2	S14469	asparagine-rich pr
57	36	46.2	247	2	H82348	hypothetical prote
58	36	46.2	294	2	T33931	hypothetical prote
59	36	46.2	301	2	AH0649	conserved hypothet
60	36	46.2	378	2	AG1313	hypothetical prote

Search completed: August 14, 2006, 15:16:36
Job time : 47 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:20:06 ; Search time 17.9412 Seconds
(without alignments)
56.277 Million cell updates/sec

Title: US-10-749-522-21
Perfect score: 78
Sequence: 1 DTEFRHSSNNFSAVR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 239914 seqs, 67312017 residues

Total number of hits satisfying chosen parameters: 239914

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_New:*

- 1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	47	60.3	28	6	US-10-890-071-53	Sequence 53, Appl
2	42	53.8	157	7	US-11-293-697-3717	Sequence 3717, Ap
3	41	52.6	35	7	US-11-055-093-211	Sequence 211, App
4	41	52.6	36	6	US-10-559-595-255	Sequence 255, App
5	41	52.6	36	7	US-11-055-093-68	Sequence 68, Appl
6	41	52.6	36	7	US-11-055-093-77	Sequence 77, Appl
7	41	52.6	36	7	US-11-055-093-210	Sequence 210, App
8	41	52.6	37	6	US-10-559-595-249	Sequence 249, App
9	41	52.6	37	6	US-10-559-595-256	Sequence 256, App

10	41	52.6	37	6	US-10-559-595-282	Sequence 282, App
11	41	52.6	37	6	US-10-559-595-283	Sequence 283, App
12	41	52.6	37	6	US-10-559-595-284	Sequence 284, App
13	41	52.6	37	6	US-10-559-595-285	Sequence 285, App
14	41	52.6	37	6	US-10-559-595-289	Sequence 289, App
15	41	52.6	37	7	US-11-055-093-45	Sequence 45, Appl
16	41	52.6	37	7	US-11-055-093-76	Sequence 76, Appl
17	41	52.6	37	7	US-11-055-093-78	Sequence 78, Appl
18	41	52.6	37	7	US-11-055-093-79	Sequence 79, Appl
19	41	52.6	37	7	US-11-055-093-80	Sequence 80, Appl
20	41	52.6	37	7	US-11-055-093-81	Sequence 81, Appl
21	41	52.6	37	7	US-11-055-093-82	Sequence 82, Appl
22	41	52.6	37	7	US-11-055-093-189	Sequence 189, App
23	40	51.3	469	7	US-11-330-403-1651	Sequence 1651, Ap
24	40	51.3	959	7	US-11-330-403-3471	Sequence 3471, Ap
25	40	51.3	959	7	US-11-330-403-4782	Sequence 4782, Ap
26	39	50.0	462	6	US-10-953-349-33642	Sequence 33642, A
27	39	50.0	477	6	US-10-953-349-33641	Sequence 33641, A
28	39	50.0	511	6	US-10-953-349-33640	Sequence 33640, A
29	38.5	49.4	715	7	US-11-056-355B-74169	Sequence 74169, A
30	38.5	49.4	718	7	US-11-056-355B-79095	Sequence 79095, A
31	38.5	49.4	719	7	US-11-056-355B-107994	Sequence 107994,
32	38.5	49.4	719	7	US-11-056-355B-119233	Sequence 119233,
33	37.5	48.1	147	7	US-11-056-355B-77122	Sequence 77122, A
34	37.5	48.1	165	7	US-11-056-355B-29319	Sequence 29319, A
35	37.5	48.1	165	7	US-11-056-355B-30964	Sequence 30964, A
36	37.5	48.1	165	7	US-11-056-355B-32909	Sequence 32909, A
37	37.5	48.1	165	7	US-11-056-355B-34554	Sequence 34554, A
38	37.5	48.1	285	7	US-11-056-355B-77121	Sequence 77121, A
39	37.5	48.1	303	7	US-11-056-355B-30963	Sequence 30963, A
40	37.5	48.1	303	7	US-11-056-355B-34553	Sequence 34553, A
41	37.5	48.1	307	7	US-11-056-355B-29318	Sequence 29318, A
42	37.5	48.1	307	7	US-11-056-355B-32908	Sequence 32908, A
43	37	47.4	36	6	US-10-559-595-288	Sequence 288, App
44	37	47.4	37	6	US-10-559-595-260	Sequence 260, App
45	37	47.4	37	7	US-11-055-093-69	Sequence 69, Appl
46	37	47.4	37	7	US-11-055-093-75	Sequence 75, Appl
47	37	47.4	805	6	US-10-449-902-55324	Sequence 55324, A
48	36	46.2	19	7	US-11-134-871-246	Sequence 246, App
49	36	46.2	36	6	US-10-559-595-263	Sequence 263, App
50	36	46.2	36	6	US-10-559-595-287	Sequence 287, App
51	36	46.2	36	7	US-11-055-093-74	Sequence 74, Appl
52	36	46.2	36	7	US-11-055-093-84	Sequence 84, Appl
53	36	46.2	37	6	US-10-559-595-257	Sequence 257, App
54	36	46.2	37	6	US-10-559-595-286	Sequence 286, App
55	36	46.2	37	6	US-10-559-595-290	Sequence 290, App
56	36	46.2	37	7	US-11-055-093-67	Sequence 67, Appl
57	36	46.2	37	7	US-11-055-093-83	Sequence 83, Appl
58	36	46.2	37	7	US-11-055-093-92	Sequence 92, Appl
59	36	46.2	37	7	US-11-244-135A-7	Sequence 7, Appli
60	36	46.2	329	6	US-10-953-349-13415	Sequence 13415, A

Search completed: August 14, 2006, 15:24:58

Job time : 22.1912 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:19:11 ; Search time 74.4118 Seconds
(without alignments)
93.375 Million cell updates/sec

Title: US-10-749-522-21
Perfect score: 78
Sequence: 1 DTEFRHSSNNFSAVR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published_Applications_AA_Main:*

- 1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	78	100.0	15	3 US-09-808-037-21	Sequence 21, Appl
2	78	100.0	15	4 US-10-162-889-21	Sequence 21, Appl
3	78	100.0	15	4 US-10-384-788-21	Sequence 21, Appl
4	78	100.0	15	4 US-10-618-856-21	Sequence 21, Appl
5	78	100.0	15	5 US-10-749-522-21	Sequence 21, Appl
6	78	100.0	15	6 US-11-073-526-21	Sequence 21, Appl
7	47	60.3	28	4 US-10-699-517-35	Sequence 35, Appl
8	47	60.3	28	4 US-10-698-099-35	Sequence 35, Appl
9	47	60.3	28	5 US-10-889-999-53	Sequence 53, Appl
10	47	60.3	28	5 US-10-890-070-53	Sequence 53, Appl
11	47	60.3	28	5 US-10-890-000-53	Sequence 53, Appl

12	47	60.3	28	5	US-10-823-463-53	Sequence 53, Appl
13	47	60.3	28	5	US-10-915-214-35	Sequence 35, Appl
14	47	60.3	28	5	US-10-822-968-53	Sequence 53, Appl
15	47	60.3	28	5	US-10-777-792-53	Sequence 53, Appl
16	47	60.3	28	5	US-10-890-071-53	Sequence 53, Appl
17	47	60.3	28	5	US-10-890-024-53	Sequence 53, Appl
18	47	60.3	28	5	US-10-928-926-53	Sequence 53, Appl
19	47	60.3	28	6	US-11-058-757-53	Sequence 53, Appl
20	47	60.3	28	6	US-11-185-907-35	Sequence 35, Appl
21	42	53.8	157	4	US-10-108-260A-3717	Sequence 3717, Ap
22	42	53.8	276	5	US-10-128-558-197	Sequence 197, App
23	42	53.8	342	4	US-10-156-761-12399	Sequence 12399, A
24	41	52.6	10	5	US-10-901-243-77	Sequence 77, Appl
25	41	52.6	10	5	US-10-901-243-78	Sequence 78, Appl
26	41	52.6	29	6	US-11-066-697-315	Sequence 315, App
27	41	52.6	29	6	US-11-066-697-328	Sequence 328, App
28	41	52.6	30	4	US-10-411-544-52	Sequence 52, Appl
29	41	52.6	30	6	US-11-066-697-310	Sequence 310, App
30	41	52.6	30	6	US-11-066-697-323	Sequence 323, App
31	41	52.6	31	3	US-09-813-345-18	Sequence 18, Appl
32	41	52.6	36	2	US-08-851-965-2	Sequence 2, Appli
33	41	52.6	36	2	US-08-851-965-30	Sequence 30, Appl
34	41	52.6	36	2	US-08-870-762A-7	Sequence 7, Appli
35	41	52.6	36	3	US-09-454-533-7	Sequence 7, Appli
36	41	52.6	36	4	US-10-649-138-7	Sequence 7, Appli
37	41	52.6	36	4	US-10-643-681-4	Sequence 4, Appli
38	41	52.6	36	5	US-10-991-597-12	Sequence 12, Appl
39	41	52.6	37	2	US-08-851-965-3	Sequence 3, Appli
40	41	52.6	37	2	US-08-851-965-29	Sequence 29, Appl
41	41	52.6	37	2	US-08-851-965-31	Sequence 31, Appl
42	41	52.6	37	2	US-08-851-965-32	Sequence 32, Appl
43	41	52.6	37	2	US-08-851-965-33	Sequence 33, Appl
44	41	52.6	37	2	US-08-870-762A-4	Sequence 4, Appli
45	41	52.6	37	2	US-08-870-762A-6	Sequence 6, Appli
46	41	52.6	37	2	US-08-870-762A-8	Sequence 8, Appli
47	41	52.6	37	2	US-08-870-762A-9	Sequence 9, Appli
48	41	52.6	37	2	US-08-870-762A-10	Sequence 10, Appl
49	41	52.6	37	3	US-09-813-345-16	Sequence 16, Appl
50	41	52.6	37	3	US-09-956-625-27	Sequence 27, Appl
51	41	52.6	37	3	US-09-454-533-1	Sequence 1, Appli
52	41	52.6	37	3	US-09-454-533-8	Sequence 8, Appli
53	41	52.6	37	3	US-09-454-533-34	Sequence 34, Appl
54	41	52.6	37	3	US-09-454-533-35	Sequence 35, Appl
55	41	52.6	37	3	US-09-454-533-36	Sequence 36, Appl
56	41	52.6	37	3	US-09-454-533-37	Sequence 37, Appl
57	41	52.6	37	3	US-09-454-533-41	Sequence 41, Appl
58	41	52.6	37	3	US-09-875-571A-1	Sequence 1, Appli
59	41	52.6	37	4	US-10-197-954-8	Sequence 8, Appli
60	41	52.6	37	4	US-10-301-488A-46	Sequence 46, Appl

Search completed: August 14, 2006, 15:23:59

Job time : 87.4118 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:15:15 ; Search time 34.4118 Seconds
 (without alignments)
 38.154 Million cell updates/sec

Title: US-10-749-522-21
 Perfect score: 78
 Sequence: 1 DTEFRHSSNNFSAVR 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : Issued_Patents_AA:*
 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	78	100.0	15	2	US-09-830-954A-21	Sequence 21, Appl
2	47	60.3	28	2	US-09-724-961-53	Sequence 53, Appl
3	47	60.3	28	2	US-09-580-018-53	Sequence 53, Appl
4	47	60.3	28	2	US-09-724-551-53	Sequence 53, Appl
5	47	60.3	28	2	US-09-724-953-11	Sequence 11, Appl
6	47	60.3	28	2	US-09-724-567-11	Sequence 11, Appl
7	47	60.3	28	2	US-09-724-940-53	Sequence 53, Appl
8	47	60.3	28	2	US-09-979-952-11	Sequence 11, Appl
9	47	60.3	28	2	US-09-585-817-11	Sequence 11, Appl
10	44	56.4	34	1	US-07-927-755A-1	Sequence 1, Appli

11	44	56.4	34	1	US-07-927-755A-2	Sequence 2, Appli
12	41	52.6	11	7	5260275-2	Patent No. 5260275
13	41	52.6	20	1	US-07-794-288D-209	Sequence 209, App
14	41	52.6	29	2	US-09-623-548A-315	Sequence 315, App
15	41	52.6	29	2	US-09-623-548A-328	Sequence 328, App
16	41	52.6	29	2	US-09-657-276-315	Sequence 315, App
17	41	52.6	29	2	US-09-657-276-328	Sequence 328, App
18	41	52.6	30	1	US-07-794-288D-208	Sequence 208, App
19	41	52.6	30	2	US-09-813-345C-18	Sequence 18, Appl
20	41	52.6	30	2	US-09-623-548A-310	Sequence 310, App
21	41	52.6	30	2	US-09-623-548A-323	Sequence 323, App
22	41	52.6	30	2	US-09-657-276-310	Sequence 310, App
23	41	52.6	30	2	US-09-657-276-323	Sequence 323, App
24	41	52.6	30	7	5260275-4	Patent No. 5260275
25	41	52.6	31	2	US-09-070-504-18	Sequence 18, Appl
26	41	52.6	36	1	US-08-477-727A-79	Sequence 79, Appl
27	41	52.6	36	1	US-08-471-675A-5	Sequence 5, Appli
28	41	52.6	36	1	US-08-892-549-7	Sequence 7, Appli
29	41	52.6	36	2	US-08-302-069A-4	Sequence 4, Appli
30	41	52.6	36	2	US-09-576-062A-4	Sequence 4, Appli
31	41	52.6	36	2	US-09-454-533-7	Sequence 7, Appli
32	41	52.6	37	1	US-07-794-288D-1	Sequence 1, Appli
33	41	52.6	37	1	US-08-233-389C-10	Sequence 10, Appl
34	41	52.6	37	1	US-08-477-727A-80	Sequence 80, Appl
35	41	52.6	37	1	US-08-446-692-66	Sequence 66, Appl
36	41	52.6	37	1	US-08-471-675A-6	Sequence 6, Appli
37	41	52.6	37	1	US-08-259-762-1	Sequence 1, Appli
38	41	52.6	37	1	US-08-259-762-4	Sequence 4, Appli
39	41	52.6	37	1	US-08-259-762-5	Sequence 5, Appli
40	41	52.6	37	1	US-08-801-863-10	Sequence 10, Appl
41	41	52.6	37	1	US-08-486-596A-10	Sequence 10, Appl
42	41	52.6	37	1	US-08-488-351A-66	Sequence 66, Appl
43	41	52.6	37	1	US-09-004-713-10	Sequence 10, Appl
44	41	52.6	37	1	US-08-892-549-1	Sequence 1, Appli
45	41	52.6	37	1	US-08-892-549-8	Sequence 8, Appli
46	41	52.6	37	1	US-08-892-549-34	Sequence 34, Appl
47	41	52.6	37	1	US-08-892-549-35	Sequence 35, Appl
48	41	52.6	37	1	US-08-892-549-36	Sequence 36, Appl
49	41	52.6	37	1	US-08-892-549-37	Sequence 37, Appl
50	41	52.6	37	1	US-08-892-549-41	Sequence 41, Appl
51	41	52.6	37	2	US-08-784-582-54	Sequence 54, Appl
52	41	52.6	37	2	US-08-302-069A-5	Sequence 5, Appli
53	41	52.6	37	2	US-09-070-504-16	Sequence 16, Appl
54	41	52.6	37	2	US-09-576-062A-5	Sequence 5, Appli
55	41	52.6	37	2	US-09-454-533-1	Sequence 1, Appli
56	41	52.6	37	2	US-09-454-533-8	Sequence 8, Appli
57	41	52.6	37	2	US-09-454-533-34	Sequence 34, Appl
58	41	52.6	37	2	US-09-454-533-35	Sequence 35, Appl
59	41	52.6	37	2	US-09-454-533-36	Sequence 36, Appl
60	41	52.6	37	2	US-09-454-533-37	Sequence 37, Appl

Search completed: August 14, 2006, 15:18:21

Job time : 44.4118 secs

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OM protein - protein search, using sw model

Run on: August 14, 2006, 15:04:09 ; Search time 59.1176 Seconds
 (without alignments)
 116.010 Million cell updates/sec

Title: US-10-749-522-21
 Perfect score: 78
 Sequence: 1 DTEFRHSSNNFSAVR 15

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1000 summaries

Database : A_Geneseq_8:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
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 5: geneseqp2002s:*
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 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*
 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	78	100.0	15	4	AAB47116	Aab47116 EFRH cont
2	78	100.0	15	6	AAO16076	Aao16076 Neurologi
3	78	100.0	15	8	ADJ88127	Adj88127 Anti-aggr
4	47	60.3	28	4	AAB46176	Aab46176 Tetanus t
5	47	60.3	28	8	ADP02901	Adp02901 Fusion pr
6	47	60.3	28	9	AEA51392	Aea51392 Abeta and
7	47	60.3	28	9	AEA62803	Aea62803 Immunocon

8	47	60.3	28	9	AEC03768	Aec03768 A-beta 1-
9	47	60.3	28	10	AEF96798	Aef96798 Human amy
10	47	60.3	33	4	AAB49075	Aab49075 Amyloid b
11	42	53.8	157	7	ADM05032	Adm05032 Human pro
12	42	53.8	157	9	AEC87962	Aec87962 Human cDN
13	42	53.8	276	7	ADE08042	Ade08042 Novel pro
14	42	53.8	276	9	ADU40412	Adu40412 Novel hum
15	41	52.6	10	2	AAR53704	Aar53704 Diabetes
16	41	52.6	10	2	AAW99230	Aaw99230 Amyloidog
17	41	52.6	10	2	AAY29577	Aay29577 Amylin am
18	41	52.6	10	7	ADF50817	Adf50817 Decamer p
19	41	52.6	10	7	ADF50818	Adf50818 Decamer p
20	41	52.6	10	8	ADR83633	Adr83633 Human IAP
21	41	52.6	10	8	ADR83634	Adr83634 Human IAP
22	41	52.6	10	9	ADV99064	Adv99064 Human IAP
23	41	52.6	10	9	ADV99065	Adv99065 Human IAP
24	41	52.6	19	3	AAV99237	Aay99237 HLA class
25	41	52.6	20	2	AAR37004	Aar37004 18His, 23
26	41	52.6	29	4	AAB91154	Aab91154 Pancreati
27	41	52.6	29	4	AAB91141	Aab91141 Pancreati
28	41	52.6	30	2	AAR37003	Aar37003 18His, 23
29	41	52.6	30	2	AAR53706	Aar53706 Diabetes
30	41	52.6	30	2	AAR50161	Aar50161 (8-37)-am
31	41	52.6	30	2	AAW99232	Aaw99232 Sub-pepti
32	41	52.6	30	2	AAY29579	Aay29579 Diabetes
33	41	52.6	30	4	AAB91149	Aab91149 Pancreati
34	41	52.6	30	4	AAB91136	Aab91136 Pancreati
35	41	52.6	30	7	ADM80671	Adm80671 Islet amy
36	41	52.6	31	4	AAE09822	Aae09822 Human amy
37	41	52.6	31	8	ADR83672	Adr83672 Amyloidog
38	41	52.6	36	2	AAR29197	Aar29197 Des-Lys(1
39	41	52.6	36	2	AAR37782	Aar37782 des-Lysl
40	41	52.6	36	2	AAY22436	Aay22436 Des-Lysl
41	41	52.6	36	3	AAB18575	Aab18575 Amino aci
42	41	52.6	36	5	ABB05488	Abb05488 Human amy
43	41	52.6	36	8	ADI36174	Adi36174 Human amy
44	41	52.6	36	8	ADO51018	Ado51018 Human amy
45	41	52.6	36	9	ADV92835	Adv92835 Amylin pe
46	41	52.6	36	9	AEB17934	Aeb17934 Human amy
47	41	52.6	36	9	AEB98244	Aeb98244 Human amy
48	41	52.6	36	9	AEB98253	Aeb98253 Human amy
49	41	52.6	36	9	AEC75159	Aec75159 Human amy
50	41	52.6	37	1	AAP82573	Aap82573 Diabetes

Search completed: August 14, 2006, 15:08:09
 Job time : 90.1176 secs